Page 1

1

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> 0 < o| |0 IntelliGenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query sequence being compared:US-09-978-385-2 (1-805)
Number of sequences searched:
4
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results file Seq2-Peps.res made by tport on Fri 28 Feb 103 11:22:23-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastDB - Fast Pairwise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                             SCORE 0|
STDEV -1
                                                                                                                                                                                                                                                                    Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                     Similarity matrix Threshold level of sim.
                                                                                                                                                                                                                                                        Randomization group
                                                      The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                       Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                      Times:
                                                                                                                                                                                                        Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100-
                            A 100% identical sequence to the query sequence was found:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Results of the initial comparison of US-09-978-385-2 (1-805) with: File : US09978385.pep
                                                                                                                                                                                                                                                                                                                                                                                                                179
Description
                                                                                                                                                             00:00:00.00
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n. 16%
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Window size
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                                                                                                                   44
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Length Score Score Sig. Frame
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7 E B X C Z

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SECNES

Sequence Name

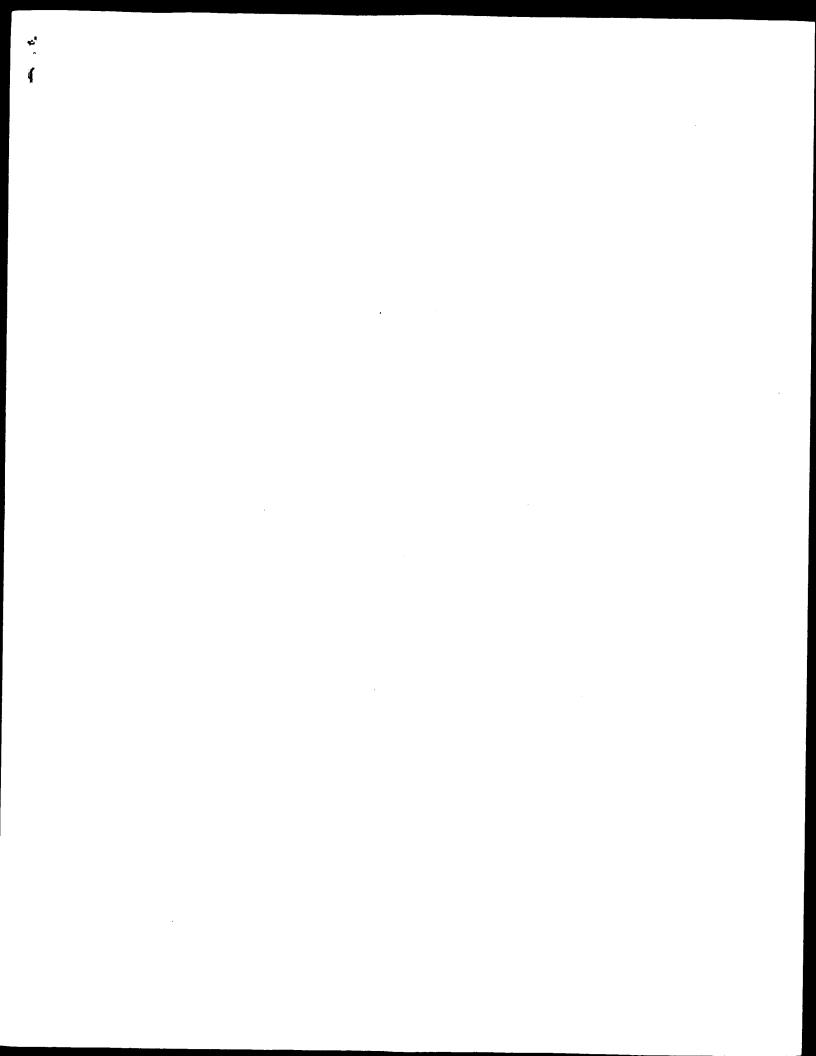
| On | 1. US-09-978-385-2 Sequence 2, Application US 805 805 805 805 | 80 AU | |
|----|---|-------|--|
|----|---|-------|--|

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Residue Identity =
2. US-09-978-385-2 (1-805)
                                             CTKVIMDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDN
                                                                               CTKVTMDNFLTAHHEMGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLPSDFQEDS
370 380 390 400 410 420 430
                                                                                                                                                                       YSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGGLPAHLLGDMWGREWTNLYSLTVPFGOK
                                                                                                                                                                 YNRNOLIEDVERTEAEIKPLYEHLHAYVRRKLMDTYPSYISPTGCLPÄHLLGDMWGRFWINLYPLTVPFAOK
                                                                                                                                                                                                       US-09-978-385-6 Sequence 6, Application US/09978385
                                                                                                                                                                                                                                                                                                                                                                                                                 PGFQNTDDVQTSF
                                                                                                                                                                                                                                                                                                                                                                                                   PGFQNTDDVQTSF
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                                                                          450
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                                                                         460
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                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                         Optimized Score =
                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                    Significance = 0.45
                                                                                                                                                                                                     200
                                           490
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Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3. US-09-978-385-2 (1-805)
US-09-978-385-9 Sequence 9, Application US/09978385
CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDN
CTKVTMDNFLTAHHEMGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLPSDFQEDS
                                                                                                                                                                   PNIDVTDAMMNOGWDAERITQEAEKFFVSVGLPHMTQGFWANSMLTEPADGRKVVCHPTAMDLGHGDFRIKM
                                                                                                                                                                                 PNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                   LKEQSTLAQMYPLQEIQNLTVKLOLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLYEGQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPRNPQECLLLYEGQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPRNPQECLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSSSSWLLLSLVAVTTAGSLTEENAKTFLINIFNGEAEDLSYGSSLASWINITUTEENAGKMSEAAAKWSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFUHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGFQNTDDVQTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGFQNSDDAQTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNMYVRDLLNYFEPLFTWLKDQNKNSFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLERSSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAMRKYFSIIKNOTVPFLEEDVRVSDLKBRVSFYFFVTSPONVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNMDVKPLLNYFQPLFDWLKEQNRNSFVGWNTEWSPYADOSIKVRISLKSALGANAYEWTNNEMFLFRSSVA
                                                                                                                                                                                                                                                                                                                                                                                                160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590
                                                                                                                                              380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751 Optimized Score = 751
81% Marches = 659
Conservative Substitutions
                                                                                                                                                                                                                              310
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| 800 X PGFQNTDDVQTSF | 730 740 750 760 770 780 780 780 770 780 770 780 770 780 770 780 770 780 770 780 770 77 | 650 650 670 680 700 710 720 YAMROYFLKVKNOMILFGEEDVRVANIKKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSHINDAFFLANN | 580 590 600 610 620 630 630 640 KNMNVPDLLNYEPLETWIKDONKNSFYGWSTDWSPYADQSIKVRISIKSALGDKAYEWNDMEMYLFRSSVA : : | 510 520 530 540 550 550 570 HVSNDYSEIRYYTRTLYQEQEQEALCQAAKHEGELHKCDISNSTEAGOKLENMERLGKSEDWTLALENIVYGA | 440 |
|---------------------|--|--|---|--|-----|
| × sa × | 740 | 670 | 590 6 (FEPLFTWLKDQ (FQPLFDWLKEQ 590 6 | 520 TRTLYQFQFQ TRTIYQFQFQ 520 | 450 |
| | 750 ILIVEGVVMGV : : LIIEGVVMAI 750 | 680 RVANLKPRISI : : RVSDLKPRVSI 680 | 600 6 QNKNSFVGWST : QNRNSFVGWNT 600 6 | 530 EALCQAAKHE EALCQAAKYN | 460 |
| | 760 IVVGIVILIF : : ,VVVGIIILIV 760 | 660 670 710 720 730 730 730 730 730 730 730 730 730 73 | 590 600 610 620 630 640 MYFEBLETWILKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGOKAYEWNDRWSPYADQSIKVRISLKSALGOKAYEWNDRWSPYADQSIKVRISLKSALGOKAYEWNDRWSPYADQSIKVRISLKSALGAKAYEWNDRWSPYADQSIKVRISLKSALGAKAYEWTNNEMFLFRSSVLLXYFQPLFDWLKEQNRRSFVGWNTEMSPYADQSIKVRISLKSALGAKAYEWTNNEMFLFRSSVLLXYFQPLFDWLKEQNRRSFVGWNTEMSPYADQSIKVRISLKSALGAKAYEWTNNEMFLFRSSVL | 540 GPLHKCDISN: GSLHKCDISN: 540 | 470 |
| | 770 : TGIKGRKKN TGIKGRKKKN | 700 VSDIIPRTEVI : VSDVIPRSEVI 700 | 620 630 KVRISLKSALGD KVRISLKSALGA 620 630 | 550 STEAGQKLFN STEAGQKLLKI 550 | 480 |
| | 780 KARSGENPYA: : ETKREENPYD: 780 | 710 EKAIRMSRSRI EDAIRMSRGRI 710 | 630 640 LGDKAYEWNDNEM LGANAYEWTNNEM 630 640 | 560 ALRLGKSEPWI ALSLGNSEPWI 560 | 490 |
| | 790 SIDISKGENN SMDIGKGESN 790 | 720 INDAFRLNDN INDVFGLNDN 720 | 10 | 570 LGKSEPWTLALENVVGA | 500 |



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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 13, 2003, 16:51:32; Search time 39 Seconds (without alignments) 2750.429 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSSSWLLLSLVAVTAAQST.....ISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-978-385-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                  SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*

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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIDSI/gcgoata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Match Length DB

| | Human PRO1885 poly | | AAU12207 | 22 | 555 | 69.4 | 2979 |
|----|-------------------------|------------|----------|----|-----------------|-------|-------|
| | Mouse Zace2-10 pro | | AAB48098 | 22 | 805 | 83.0 | 3561 |
| | Mouse Zace2-5 prot | | AAB48097 | 22 | 805 | 83.4 | 3579 |
| | Novel human protei | | AAU09092 | S | | 88.0 | 3775 |
| | Human ACE-2 full-1 | | AAE20353 | 23 | 805 | 100.0 | 4291 |
| | Human angiotensin | | AAU99701 | 23 | 805 | 100.0 | 4291 |
| | Human Zace2 protei | | AAB48095 | 22 | 805 | 100.0 | 4291 |
| | Human angiotensin | | AAY72667 | 22 | 805 | 100.0 | 4291 |
| | Human MPROT15 amin | 22-01-1849 | AAY67310 | 21 | 805 | 100.0 | 4291 |
| | A human angiotensi 3000 | 00-04-2000 | AAY84562 | 21 | 805 | 100.0 | 4291 |
| 7. | Description | | ID | BB | Match Length DB | Match | Score |

1000/054321

| 376 | 380 | 381 | 381 | 381 | 381 | 381 | 381 | 381 | 381 | 381 | 383 | 384 | 387 | 409.5 | 476 | 502.5 | 656 | 715.5 | 735 | 841 | 990 | 990 | 990 | 1028 | 1057 | 1086 | 1334 | 1334 | 1336 | ω | ω | 1344 | 5 | 53 |
|-------------------|----------|----------|----------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|----------|----------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|----------|--------------------|--------------------|
| | | | | | | | | * | | 8.9 | | | • | | • | 11.7 | 15.3 | 16.7 | • | 19.6 | | 23.1 | | 24.0 | • | • | • | • | • | | • | 31.3 | • | • |
| 184 | 223 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 222 | 628 | 611 | 661 | 252 | 465 | 235 | 792 | 694 | 694 | 694 | 630 | 660 | 615 | 1252 | 1249 | 1306 | 1306 | 1265 | 732 | 261 | 480 |
| 22 | 21 | 21 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 19 | 22 | 22 | 22 | 22 | 23 | 22 | 22 | 22 | 23 | 22 | 21 | 22 | 16 | 22 | 22 | 22 | 19 | 11 | 23 | 12 | 22 | 21 |
| AAM23565 | AAY76135 | AAG00014 | AAY04156 | AAY01594 | AAY12986 | AAY12680 | AAW93620 | AAY35890 | AAY25459 | AAY59653 | AAY04174 | AAW29670 | AAB88580 | ABB59496 | ABB70388 | ABB59152 | AA020950 | AAG67296 | AAU25463 | ABB71128 | ABB09432 | AAU08701 | AAY93619 | ABB65165 | AAR70013 | ABB64006 | AAU02985 | AAU02957 | AAW68155 | | AA020501 | AAR10426 | 091 | AAY67311 |
| Human EST encoded | н | secreted | • | d prot | creted | Human 5' EST secre | ESTS | Ω | Human secreted pro | | | Homo sapiens clone | oph | Drosophila melanog | | | | | Human mddt protein | | \vdash | Human zinc metallo | | Drosophila melanog | × | Drosophila melanog | Angiotensin conver | Angiotensin conver | Human angiotensin | Human angiotensin | Protein of APP rel | Ė | Novel human protei | Human MPROT15 amin |

ALIGNMENTS

RESULT 1 AAY84562 A human angiotensin converting enzyme-2 (ACE-2) protein. 25-JUL-2000 (first entry) AAY84562; AAY84562 standard; Protein; 805 AA

Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9); BIGGD pressure; hypertension; congestive hears failure; atherosclerosis; chronic heart failure; acute heart failure; myocardial infarction; renal failure

Homo sapiens.

Domain Domain Domain Domain Peptide Key 19..740 /note= "extracellular domain" 374..378 741..765 /note= "transmembrane domain" 766..805 Location/Qualifiers /note= "minimal zinc binding domain" /note= "signal sequence" 'note= "cytoplasmic domain"

XX PN FT WO200018899-A2

06-APR-2000

29-SEP-1999;

98US-0163648 99WO-US22976.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The sequence of the full length ACE-2 CDNA was determined from a clone obtained from a cDNA library prepared from mRNA of a human heart of a subject who had congestive heart failure. ACE-2 has significant sequence homologies with ACE enzymes, and has also been shown to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure related diseases and conditions, such as hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosclerosis and renal
                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 1; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2) polypeptide useful for detecting an ACE-2 therapeutic for treating hypertension, congestive heart failure, myocardial infarction,
                                                                                                      421
                                                                                                                                       421
                                                                                                                                                                      361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acton LS,
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                                                KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQFQEALQQAAKHEGPLH
KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                                                             CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                                                                                 AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                                                                             HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
                                                                                                                                                                                                                                                                                                                                                                             EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVBHTFEBIKPLYEHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ
                                                                                              IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                                                                AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                                                            HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60

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           Query Match
Best Local 9
                                                           This is amino acid sequence #1 of human MPROT15. The MPROT15 polynucleotide and polypeptide sequences can be used for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing of peptide hormones and cytokines.
                                                                                                                                         MPROT15 polypeptide and MPROT15 polynucleotides - useful for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease etc.
                                           Sequence
                                                                                                                         Claim 1; Page 15; 22pp; Japanese.
                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                             MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                       13-MAY-1998;
18-AUG-1998;
                                                                                                                                                                                                                                                                       22-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      heart disease; apopl
Alzheimer's disease;
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           Similarity
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98GB-0018009
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         100.0%;
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; Score 4291;
; Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                  Human angiotensin converting enzyme-2 (ACE-2).
                                                                                                           Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase screening; therapy; hypertension; congestive heart failure; CHF;
                                                                                                                                                                                31-MAY-2001
                                                                                                                                                                                                                                                                                                781
                                                                           Homo sapiens
                                                                                                   inflammation; pain.
            Protein
                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEINSLSAATPKHLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                 QMILEGEEDVRVANLKPRISENFEVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWYVFKGEIPKDQWXKKWWEM
                                                                                                                                                                                                                                                                                                                                                                                                                        QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN 660
                                                                                                                                                                                                                                                                                                                                              SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YASIDISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                                                                                                                              YASIDISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                 (first entry)
/label= Signal_peptide
19..805
/label= Mature_ACE-2_protein
                                                   Location/Qualifiers
                                                                                                                                                                                                                                     805 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence is human angiotensin converting enzyme-2 (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart ACE-2 antagonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 injection for determining the disease or condition associated with a horizont reversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel genes encoding angiotensin converting enzyme-2 useful as antisense or antigene agents for therapeutics, diagnostics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-210604/21.
N-PSDB; AAD02758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening assays .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an aberrant protein level.
                                                                                                                                                                                                                                   121 NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                301 AWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
                                                                                  241 HAYVRAKLMNAYPSXISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPNIDVTDAMVDQ
                                                                                                                                  181 EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                      1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
                                                                                                                                                    EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                     NIMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
                                                                                                                                                                                                                                                                                                   NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                     NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/label= TMD
/note= "Transmembrane domain; Hydrophobic region"
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/label= ZBD
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                                     Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
 Example 1; Page 95-100; 125pp; English.
                     bowel disease, e.g. Crohn's disease and ulcerative colitis, or disease arthritis and enterocolitis
                                                                                            N-PSDB; AAC84366, AAC84367.
                                                                                                             WPI; 2001-025018/03.
                                                                                                                                         Piddington CS,
                                                                                                                                                                                                                                                                                                                                               Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; human; antiarthritic; bradykinin inactivator.
                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                              03-MAY-2000;
                                                                                                                                                                                                13-MAY-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                        WO200070032-A1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Zace2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB48095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB48095 standard; Protein; 805 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 YASIDISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP 780
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                                                                                                                                                                                                                                           2000WO-US11932
                                                                                                                                      Petrie CR,
                                                                                                                                                                                            99US-0311482
99US-0384706
                                                                                                                                   Shoemaker KE,
                                                                                                                                  Bishop PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                     661 QMILFGEEDVRVANLKPRISFNFEVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                                                                                                                                                             541 KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNWNVRPLLNYFEPLFTWLKDONK 600
                                                                                                                                                                                                                                           481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYOFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                                                                                  421 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGBIPKDQWMKKWWEM
                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zace2 gene in a biological sample, as probes for in vivo diagnosis and to detecting and localizing Zace2 gene expression in tissue samples, Zace2 gene, and to detect aberrations associated with the Zace2 locus. Conditions of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infertility. The present sequence represents the human Zace2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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                                                             NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
                                                                                                NSFYGWSTDWSPYADQSIKYRISLKSALGDKAYEWNDNEMYLFRSSYAYAMRQYFLKYKN 660
                                                                                                                                                                                                                    KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHBGPLH 540
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                                                                                                                                        KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 600
CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                                                                                                                                                       IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disorder; peptide hormone; cytokine processing; myocardial infarction; cardiomyopathy; inflammatory bowel disease; systemic inflammation response syndrome; polytrauma; pain; stroke; bone destruction; rheumatoid arthritis; osteoarthritis; asthma; periodontal disease; dysmenorrhoea; premature labour; brain oedema; focal injury; diffuse axonal injury; reperfusion injury; scar formation; cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss; lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis; familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia; aberrant metabolic rate; heart failure; left ventricular hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU99701 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human angiotensin converting enzyme-2 (ACE-2) protein.
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The present invention describes a new method of treating a body weight disorder, increasing muscle mass and decreasing body fat by administration of angiotensin converting enzyme (ACE)-2 modulating compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a state associated with lipid metabolism. The method is used for treati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOY-2000: 2000US-0704216.
29-MAY-2001; 2001US-0870382.
19-OCT-2001; 2001US-371741P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2001; 2001WO-US45703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200239997-A2
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                                                                                                                                                                                                                                                                                                            administering angiotensin converting enzyme-2 modulating
                                                                                                                                                                                                                                                                                                                                                    Treating body weight disorder and increasing muscle mass comprises
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK87623
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-547572/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult respiratory distress syndrome; wound healing; appetite;
                                                                                                                                                                                                                                            Example 5; Page 387-390;
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19..805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gould AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solomon
                                                                                                                                                                                                                                            395pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dales NA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown JA;
                                                                                                                                                                                                                                                                                                                       compound
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia, generalised partial lipodystrophy, familial partial lipodystrophy, hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate, congestive heart failure, chronic heart failure, left ventricular hypertrophy, acute heart failure, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease and Huntington's disease), alzheimer's disease, Parkinson's disease and Huntington's disease), diseases associated with peptide hormones or cytokine processing, myocardial infarction, cardiomyopathy, systemic inflammation response syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis
                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                           CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                                                                                                                                                                       AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEYGKQLRPLY 180
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                                                                                                                                                                                                                                                     CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                                                                                                                                                                                               AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDERILM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY
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                   KCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                      KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
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NSFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN

NSFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN

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RESULT 6
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                                The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polypucleotides. ACE-2 is also known as peptidyl dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, caute heart failure, myocardial infarction, atherosclerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility.
                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Isolated human polypeptide, known as angiotensin converting enzyme-2, useful for treating or preventing the development of an abnormal bloopressure or related diseases, e.g. hypertension, heart failure or myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD32586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
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                 present sequence is human full-length ACE-2 protein.
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                                                                                     AAU09092 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                          KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
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Pred. No. 0;
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Novel human protein NHP #1

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Huntington's disease; schizophrenia; mania; dementia; paranola; panic disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; immune system disorder; Hashimoto's thyroiditis; musculo-skeletal system disorder; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS; immunogen; acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; oifactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cachexia; male infertility; impotence; testicular cancer; lung tumour; hyperproliferative disorder; pulmonary system disorder; central nervous system disorder; bohe disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant; antinanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal disorder; cardiovascular disorder; hypertension;
coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; nootropic; antiparkinsonian; anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; novel human protein; NHP; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2000; 2000US-194118P.
29-SEP-2000; 2000US-236384P.
                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-2001; 2001WO-US10542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200174896-A1
Claim 11; Page 298-301; 318pp; English
                                                                disorders, autoimmune disorders and reproductive disorders
                                                                                            New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular
                                                                                                                                                                                                    N-PSDB; AAS14880
                                                                                                                                                                                                                                       WPI; 2001-626394/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
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                                                                                                                                                                                                                                                                                                           Dillon PJ;
                                                                                                                                                                                                                                                                                                                                        Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Other= Any amino acid encoded by WST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Other= Any amino acid encoded by RCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
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/note= "Other= Any amino acid encoded by NTT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Immunogenic_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Immunogenic_epitope
                                                                                                                                                                                                                                                                                                                                    Soppet DR, Coleman TA, Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel human proteins (NHP) and the nucleic acids that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, prognosis, prevention and/or treatment or diseases and/or disorders involving vasoconstriction, gastrointestinal disorders, cardiovascular disorders (e.g. hypertension, erectile dysfunction, high blood pressure, coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia, cachexia, disorders of small intestine, disorders of reproductive systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (e.g. male infertility and/or impotence), testicular cancer, lung tumours and other hyperproliferative disorders, disorders of pulmonary system, central nervous system disorders, bone disorders, neurodegenerative diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, panic disorder, learning disabilities, amyotropic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sepsis, acne, psoriasis and lupus erythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound healing. The present sequence represents an NHP of the invention the gene for which is located on the X chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    central nervous system disorders (e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psychoses, autism, sleep disorders), immune system disorders (e.g. Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TKVTNDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
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                                                                                                                                                                                                                                                                                                                                                                                     422 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK
662 MILEGBEDVRVANLKPRISENFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNS 721
                                                                     62 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120
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                                                                                                                                                              CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540
                                                                                                                                                                                                                                                                              REIVGVVEPVDHDETYGDPASLFHVSNDYSFIRYYTRTLYGFQFQBALCQAAKHEGPLHK 541
                                                                                                                                                                                                                                                                                                                                          CDISNSTEAGOKLFNMLRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 601
                                                                                                                                                                                                                                                    REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
                                                                                                                SFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711 AA;
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1; Mismatches 4; 7 Indels 0
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The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an disease associated with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory modulecules. The nucleic acids can be used to detect the expression of a
                                                                                                                                                                               Angiotensin-converting enzyme, zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                           Claim 7; Page 104-109; 125pp;
                                                                                                                                                                                                                                              N-PSDB; AAC84368, AAC84369.
                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                           27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                      13-MAY-1999;
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                                SLEFLGIHPTLEPPYOPPYTWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREENP
                                                                   SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
                                                                                                          QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                              NSFYGWNTEWSPYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKN
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RESULT 9
AAB48098
Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse; antiarthritic; bradykinin inactivator.
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27-AUG-1999;
                                                                                                                                                         The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), disease associated with inflammation like arthritis and enterocolitis,
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                                            as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory incledules. The nucleic acids can be used to detect the expression of a molecules in a biological sample, as probes for in vivo diagnosis and for detecting and localizing zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the
                                                                                                                                                                                                                                                                                                        Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                          Piddington CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                            Claim 7; Page 113-118; 125pp; English.
Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive
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RESULT 10

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                  YASIDISKGENNPGFQNTDDVQTSF 805
                                                                                                      SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
                                                                                                                                      QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVTPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                                                                        QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
                                                                                                                                                                                                                                                                                  KCDISNSTEAGQKLIKMLSLGNSEPWTEALENVVGARNMDVKPLLNYFQPLFDWLKEQNR
                                                                    SLEFLGIHPTLEPPYQPPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREENP
   YDSMDIGKGESNAGFQNSDDAQTSF
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Pred. No. 2.
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AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from
                                                                                                                                                              Claim 12; Fig 72; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
01-MAR-2000;
21-MAR-2000;
31-MAR-2000;
31-MAR-2000;
                                                                                                                                                                                            Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
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11-FEB-2000;
18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                             Stewart TA,
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2000WO-US08439
2000WO-US13705
2000WO-US14042
2000WO-US14941
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2000WO-US07377.
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L, Sherwood S;
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                                        Alzheimer's disease; cytokine.
                                             MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
heart disease; apoplexy; heart disease; nervous denaturation; hormone;
                                                                                                                                            11-APR-2000 (first entry)
                                                                                                         Human MPROT15 amino acid sequence #2.
                                                                                                                                                                                                             AAY67311 standard; Protein; 480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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99.8%;
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Pred. No. 3.8e-244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 20-21; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                            AAU09102 standard; Protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWS 70
                                                                                                                                                                                                                                                                                                   310
                                                                                                                                                                                                                                                                                                                              311 AEKFFYSYGLPNMTQGFWENSMLTDPGNYQKAYCHPTAWDLGKGDFRILMCTKYTMDDFL 370
                                                                                                                                                                                                                                                                                                                                                              250 AYPSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 309
                                                                                                                                                                                                                                                                                                                                                                                           251 AYPSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDYTDAMYDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                           190 ARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AFLKEOSTLAOMYPLOEIQNLTVKLOLOALOONGSSYLSEDKSKRLNTILNTMSTIYSTG 130
Novel human protein NHP #11.
                                20-DEC-2001
                                                                AAU09102;
                                                                                                                                                                                                     431 DNETEINFLLKQALTIVGTLPETYMLEKWRWMVEKGEIPKDQWMKKWWEMK 481
                                                                                                                                                                                                                                   370 TAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQE
                                                                                                                                                                                                                                                                371 TAHHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEINSLSAATPKHLKSIGLLSPDFQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide hormones and cytokines.
                                                                                                                                                                        430 DNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEBIKPLYEHLHAYVRAKLMN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVLKNEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEYGKQLRPLYEEYYVLKNEM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTG 129
                                                                                                                                                                                                                                                                                                 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-0010373.
98GB-0018009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0014949
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.2%; Score 2539; DB 21; 100.0%; Pred. No. 7.4e-207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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disorders (e.g. hypertension, erectile dysfunction, high blood pressure, cachearly heart disease and arteriosclerosis), anorexia, obesity, bulimia, cachearly heart disease and arteriosclerosis), anorexia, obesity, bulimia, cachearly, disorders of reproductive system cachearly, disorders of reproductive system cachearly, disorders, disorders of reproductive system, can do ther hyperproliferative disorders, disorders of pulmonary system, can defense and behavioural disorders, bone disorders, neurodegenerative cachearly carning ton's disease, schizophrenia, mania, dementia, paranoia, cadisease, Huntington's disease, schizophrenia, mania, dementia, paranoia, cadisease, huntington's disease, schizophrenia, mania, dementia, paranoia, capandidisorders (e.g. panic disorders (e.g. humune system disorders (e.g. psychoses, autism, sleep disorders), immune system disorders (e.g. psychoses, autism, sleep disorders), immune system disorders, cachearly cachearly infectious disease, diabetes mellitus, cachearlia, rheumatoid arthritis, inflammatory bowel disease, capania, acquired immunodeficient syndrome cachearly, included arthritis, inflammatory bowel disease, capania, acquired immunodeficient syndrome special acceptance, cachearly, neural system cachearly, respiratory disorders, olfactory disorders and wound disorders, respiratory disorders, olfactory disorders and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperpoliferative disorder; pulmonary system disorder; hyperpoliferative disorder; bone disorder; central nervous system disorder; bone disorder; barkinson's disease; neurodegenerative disease; Alzheimer's disease; parkinson's disease; huntington's disease; schizophrenia; mania; dementia; paranola; parlic disorder; learning disability; amyotropic lateral sclerosis; panic disorder; learning disorder; immune system disorder; psychosis; altism; sleep disorder; immune system disorder; psychosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; immunological disorder; asthma; AIDS; immunological disorder; asthma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; novel human protein; NHP; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary; neuroprotective; nootropic; antiparkinsonian; anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia; cachexia; male infertility; impotence; testicular cancer; lung tumour cachexia; male infertility; impotence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
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29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-2001; 2001WO-US10542.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel human proteins (NHP) and the nucleic acids that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, proyention and/or treatment or diseases and/or disorders prognosis, prevention and/or treatment or diseases and/or disorders involving vasoconstriction, gastrointestinal disorders, cardiovascular involving vasoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 311-312; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS14890.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-626394/72.
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Dillon PJ;
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2000US-236384P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coleman TA, Gentz RL,
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RESULT 13
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A bank of human testicular cDNA in Lambda gtll was screened with a probe containing the final 3248 nucleotides of endothelial ACE. The complete sequence of tACE was reconstructed from 4 separate clones.
                                                                    Nucleic acid - encoding human testicular angiotensin conversion enzyme, used e.g. for in vitro detection of enzyme in organism
                                                       Claim 1; Fig 1; 48pp; French.
                                                                                                                     N-PSDB; AAQ10328
                                                                                                                               WPI; 1991-036748/05.
                                                                                                                                                Soubrier F, Alhenc-Gelas F, Hubert C,
                                                                                                                                                                          (INRM ) INST NAT SANTE RECH
                                                                                                                                                                                                     05-JUL-1989;
                                                                                                                                                                                                                             05-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                    10-JAN-1991.
                                                                                                                                                                                                                                                                           W09100354-A.
                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          human testicular angiotensin conversion enzyme; tACE;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human testicular angiotensin conversion enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR10426 standard; Protein; 732 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 WDAQRIFKEAEKF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 WDAQRIFKEAEKF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKFNIDVTDAMVDQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 AYVRAKLMNAYDSYISPIGCLPAHLLGDMWGRFWTNLYSLTVDFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGYDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healing. The present sequence represents an NHP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNNAGDKWSAFLKEGSTLAOMKPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
                                                                                                                                                                                                 89FR-0009062.
                                                                                                                                                                                                                        90WO-FR00513
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                                                                                                                                                                                                                                                                                                            /label= signal peptide 22..732
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                           /label= mature tACE
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1359; DB 22;
Pred. No. 5.3e-107;
                                                                                                                                               Corvol P;
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RESULT 14
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                                        640 LHGEKLGWPQYNWTPNSARS 659
                                                                            601 --NSFVGW-STDWSPYADQS 617
                                                                                                                                541 KCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNVFEPLFTWLKDONK 600
                                                                                                                                                                        520 RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH 579
                                                                                                                                                                                                           481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                               461 LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                                                                   421 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                                                                       401 CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS 460
                                                                                                                                                                                                                                                                                                                                               361 CTKVTMDDFLTAHHEMGHTQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                341 WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                  302 WDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 YVELINQAARLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The isolated nucleic acid sequence was inserted into a plasmid for expression of the protein. The invention covers polypeptides containing all or part of tACE sequence. These are useful in pancreatment of inflammation or infectious diseases, especially acute pancreatitis, or diseases in which kinins are involved. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 METTYSVATVCHPNG--SCLOLEPDLTNVMATSRKYEDLLWAWBGWRDKAGRAILQEYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWBSWRSEVGKOLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALÞAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against the polypeptides are useful as immunoassay reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 NNAGDKWSAFLKEOSTLAOMYPLOEIONLTVKLOLOALOONGSSVLSEDKSKRLNTILNT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TSAQSPNIVTDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 TAAOS----TIEEOAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVONM 62
                                                                                                KCDIYQSKEAGORLATAMKLGFSRPWPEAMQLITGOPNMSASAMLSYFKPLLDWLRTENE 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Score 1344; DB 12; Length 732; Lonservative 119; Mismatches 204; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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XX DE XXX
APP pathway modulator; gene therapy
   Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human App;
                                                        Protein of APP related human homologue hCP51674.
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27-JUN-2002 (first entry)

AAO20501;

AAO20501 standard; Protein; 1265 AA

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                                                                                                                                                                                                                                                                   Matches 255;
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001; 2001WO-EP11345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200226820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-2000;
14-JUN-2001;
                                                                                                                                                                                                                                                                                                                                              specific expression control sequence. Expression of the sequence gives the fly an altered phenetype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonucleotide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used stranded RNA molecule, ribozyme, or particularly an antibody. It is used as to treat conditions such as Alzheimer's disease. The agent can be used as to pathway modulator or in gene therapy. This sequence represents the protein of the APP related human homologue hCP51674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid encoding a polypeptide having the Abeta portion of human amyloid encoding a polypeptide having the Abeta portion of human amyloid encoding polypeptide having the a signal sequence. The DNA sequence encodes a 123 (Abeta 40) or 129 (Abeta 42) amino acid sequence, given it the specification. The DNA sequence is operably linked to a tissue-the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reinhardt MWHM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 94-97; 129pp; English.
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                           603 TDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT----- 656
                                                                                                                          132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVLKNEMA 191
                                                                                                                                                     657 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 714
                                     773 RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH 822
               252
                                                                                                                                                                                                                                     20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-315796/35.
                                                                                             VCHPNG---SCLQLEPDLINVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 772
                                                                                                                                                                                FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                   RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
            Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK99395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dengler UJ,
                                                                                                                                                                                                                                                                                                                            1265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-298309P
                                                                                                                                                                                                                                                                     Conservative 118; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-236893P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
/note= "Encoded by CNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zusman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= unknown
                                                                                                                                                                                                                                                                                    31.2%; Score 1337; DB 23; Length 1265; 41.7%; Pred. No. 4.6e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finelli AL, Freuler F,
         1::1 1:11: 1 1 :1:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Konsolaki M;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                  9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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                   В
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     823 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122 AGORLATAMKLGFSREWPEAMOLITGOPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1062 PVPRTQGDEDPGAKEHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 ADDFFTSLGLLPVPPEFWNKSMLEKPIDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR04111 standard; peptide; 1306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182 QYNWTPNSARS 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human angiotensin converting enzyme (ACE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR04111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 AGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLETWLKDQNK--NSFVGW- 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human angiotensin converting enzyme; hypertension; bradykinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 STDWSPYADQS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                              Modified-site
                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 30..1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="derived from pre-ACE by removal of signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=mature ACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                          /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                    /label=pitative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                               'label=putative N-glycosylation site
                                                                                                                                                                                                              /label=putative N-glycosylation site
                                                                                                                                                                                                                                                        /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                               /label=putative N-glycosylation site
/label=putative N-glycosylation site
                                                                                                                         /label=putative N-glycosylation site
                                                                                                                                                                       /label=putative N-glycosylation site
                                         /label=putative N-glycosylation site
                                                                                    'label=putative N-glycosylation site
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Matches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                 1103 PVPRTQGDFDFGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGFLHKCDIYQSKE 1162
550 AGQKLFNMLRLGKSEFWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSFVGW- 606
                                                                                                    1044 SD-EHDINFLMKMÁLDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWNSLRLKYQGLCP 1102
                                                                                                                                      430 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                         984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG
                                                                                                                                                                                                370 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                              924 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
                                                                                                                                                                                                                                                                              311 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRTLMCTKVTMDDF 369
                                                                                                                                                                                                                                                                                                                 864 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLYVPFPSAPSMDTTEAMLKQGWTPRRMFKE 923
                                                                                                                                                                                                                                                                                                                                               252 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                      814 RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human angiotensin converting enzyme hydrolyses angiotensin I and kinins. Either intact enzyme or fragments thereof can be used to generate antibodies for diagnostic use. Oligonucleotide probes can also be made
                                                                                                                                                                                                                                                                                                                                                                                                                    192 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 VCHPNG--SCLOLEFDLTNYMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which are complementary to the sequence encoding the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; ; p; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding human angiotensin converting enzyme used eg in diagnosis of hypertension, evaluation of enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 TDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNWQIANHT----- 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-132272/17.
N-PSDB; AAQ04027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INRM ) INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1990
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                                                       PVPHDETYCDPASLFHYSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88FR-0012620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=putative N-glycosylation site
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1225..1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.2%; Score 1337; DB 11; 41.7%; Pred. No. 4.8e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hubert C, Corvol P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1306;
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В

Sequence

1306 AA;

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invention to identify individuals possessing a certain genotype and cassociated ailment, and to determine if the health of that comprises identifying individuals having a certain genotype and comprises identifying individuals having a certain phenotype. Cc with the phenotype, and instituting a lifestyle change to exploit conteract the phenotype expressed by the gene marker. If the crossory is hypertension, the gene marker is at least one conteraction (I) ACE allele and exercise training is instituted to decrease systolic and diastollc blood pressure. The gene marker cappropriate gene region. The general method can be used to content you before the general method can be used to can also to identify those who are likely to be successful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
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                                                                                                                                                                                                             This is human angiotensin converting enzyme (ACE). (see AAV41320) is polymorphic with 2 common alleles resulting in 3 genotypes, II, ID and DD. It is an olymorphic not of invention to identify individuals possessing a certa
                                                                                                                                                                                                                                                                                    Disclosure; Page 35~41; 61pp; English.
                                                                                                                                                                                                                                                                                                                 angiotensin-converting enzyme genotype
                                                                                                                                                                                                                                                                                                                       Analysis of genetic markers to identify subjects who will benefit from exercise - also assessing risk of cardiovascular disease from
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV41320.
                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrell RE, Hagberg JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme; ACE; hypertension; exercise; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human angiotensin converting enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW68155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Sig_peptide
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                                                                                                                                                                                                                                                    The ACE gene
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Length 1306;

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PN SEARCH SEARCH
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                                                                                                                                                                                                                                   Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT----- 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #57.
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WO200136632-A2
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                                                                                                                                                                   vascular disorder; asbestosis.
                                                                                                                                                                                                        nonarcoidotic pulmonary granulomatous disease; endothelial abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Local

Similarity

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Query Match
                                                                                                                                                                                                                                                                                                   The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 2000WO-IL00766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                                                                       disorders including cardiovascular diseases such as arteriosclerosis, mycardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, muscular deseases such as hypertrophy, muscular deseases such as hypertrophy, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 57; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS06057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levine Z, David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                          polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-336004/35.
                                                           1249 AA;
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99IL-0133455
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31.1%; Score 1334; DB 22; 42.6%; Pred. No. 8.1e-104;
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997 HIQYEMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 TIEEQAKTFLOKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 766
                                            HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                       DGPTPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 936
                                                                                                                                                                                                                                                                                                                          GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                                                                                                                                                                                                                                                                                                                      ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                           GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 996
                                                                                                                                                                                                                                 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                              GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 876
                                                                                                                                        {\tt GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255;
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AAU02985
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                                                                                                                                                                The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen p53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                          disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antiboo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 85; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; wasoactive intestinal polypeptide receptor 2; arteriasclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
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10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular disorder; asbestosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #85
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sarcoidosis, nonarcoidotic pulmonary granulomatous diseases
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99IL-0133455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
23-MAR-2000;
11-JUL-2000;
                                                  23-MAR-2001; 2001WO-US09231.
                                                                                                                                                        Drosophila melanogaster
                                                                                       27-SEP-2001.
                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 18810.
                                                                                                                                                                                                                                                                                                                                                   ABB64006 standard; Protein; 615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   1176 MKLGYSKPWPEAMKLITGOPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 1233
                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                        ABB64006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              767 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA
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2000US-191637P
2000US-0614150
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Pred. No. 8.1e-104;
.2; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1252;
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0.840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 18810; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL08109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 KLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ
                                                                                                                                                                                                                                                                                                      365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
599 N--KNSFVGWST 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKVKVCDYKDSTKCDLALDPEIEEVISKSRDHEELAYYWREFYDKAGTAVRSQFERYVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLATLAVTQALVKEEIQAKEYLENLNKELAKRTNVETEAAWAYGSNITDENEKKKNEISA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTKAAKLNNETSGAEAWLDEYE------DDTFEQQLEDI---FADIRPLYQQIHGYVRF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGKYCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEYGKQLRPLYEEYYVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF 127
                                                                                                                                                                                                                                                                                                                                                                                                                RLRKHYGDAVVSETGPIPMHLLGNMWAQQWSEIADIVSPFPEKPLVDVSAEMEKQGYTPL 297
                                                                                                                                                                                       K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEY 476
                                                                                                                                                                                                                                                                                                TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424
                                                                                                                                                                                                                                                                                                                                        KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLTDDVRIKQCTRV
                                                                                                                                                                                                                                                                                                                                                                          RIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKV 364
                                                                       LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQ
                                                                                                                                                   VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP
                                                                                                                                                                                                                         SPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484
                                     LDNCDIYGSAAAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE
                                                                                                               SGIEPPVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP 536
                                                                                                                                                                                                                                                                TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.3%; Score 1086; DB 22
36.4%; Pred. No. 3.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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           RESULT 20
AAR70013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tick; antigen; carboxypeptidase; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tick carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR70013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70013 standard; Protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boophilus microplus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 NIKNNVHIGWTT 608
     Clone A5 was prepd. from adult tick cDNA library. Clone 4UI was prepd. from the larval stage of B. microplus (Calliope strain).

AAQ82948 is a hybrid of sequences from clone 4UI (nt 1-966 & 1747-2047) and A5 (nts 967-1746). The translation of the tick carboxypeptidase cDNA sequence is shown in AAR70013. All the native tick carboxypeptidase sequences listed in Table 11 (see AAR70014-R70023) are found in the translation (see FT). The predicted AA sequence agrees with the peptide sequence for all peptides with 2 exceptions. These differences are Asp for Gln14 in peptide T9126, and Asn for Saspl2 in peptide T9118. Tick carboxypeptidase has a mol. wt. 75172.
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                                                                                                                                                                                                                     Disclosure; Fig 6; 138pp; English.
                                                                                                                                                                                                                                                                        New antigenic tick carboxypeptidase and corresp. DNA - are used in vaccines for producing antibodies against ticks, insects and
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ82948
                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-090905/12.
                                                                                                                                                                                                                                                                                                                                                                                            Cobon GS,
                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOT-) BIOTECH AUSTRALIA PTY LTD.
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
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                                                                                                                                                                                                                                                                                                                                                                                            Kemp DH,
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639..655
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/note= "putative"
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613 KNEVVGW 619
                                                                                                                               553 HECDIYGEKNAGDVLKKGLSLGRSKPWPDVLEIMAGTROMSASSLKKYYEPLEKWLDERI 612
                                                                                                                                                                                           540 HKCDISNSTEAGGKLFNMLRLGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDQN 599
                                                                         600 KNSFVGW 606
                                                                                                                                                                                                                                                                                                         493 KYQGVSPPVKRNESFFDGGAKYHVALHVPYLRYFVAFILQFQFHEHLCTVAKKVDEHHPF 552
                                                                                                                                                                                                                                                                                                                                                                                  483 EIVGVVEPVPHDETYCDPASLFHYSNDYSFIRYTRTLYQFQFQEALCQAAK---HEGPL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 LLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 DPSVEELRTVHHEMGHIEYYMQYKHLHVLLQEGANEGFHEAVGDLIALSVATKTHYGKLS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AQKMFHAAEDFFTSLGLDNMTSEFWSKSILTKPED-REIQCHASAWNMYNGDDFRIKMCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 KVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In addition to the features in FT, the carboxypeptidase AA sequence has 8 potential N-lined glycosylation sites and a potential glycosylphospatidyl inositol anchor sequence similar to that found in Bm86. It has significant homology with zinc dependent dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDDGNVQKAVCHPTAWDLGKG-DFRILMCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLY-SLTVPFGQKPNIDVTDAMVDQAWD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 KLSNEAASLDGYDNIKSAWLSDYETE-----NMTEIVDKLWEDLSPLYKKLHAYV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 VLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 GSTKVTVGKDKDLP-----LEPDLTRNMKEVGNYDKLLQTWLAWHNAVGPAIKQYYIPYI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 STGKVC---NPDNPQECLILLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYV 184 : | | : : | | :: | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | : : | | : : | : : | | : : | : : | | : : | : : | : : | | : : | : : | | : : | : : | | : : : | | : : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : : | : : : | : : : | : : : : | : : : | : : : | : : : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LVAVTAAQSTIEEQAK--TFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNN-AGD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 AA;
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```

Search completed: March 13, 2003, 16:56:56 Job time : 50 secs

```
GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 13, 2003, 16:56:13; Search time 20 Seconds (without alignments) (without alignments)

Sequence:

1 WS-09-978-385-2

Perfect score: 4291
Sequence:

1 MSSSSWLLLSLVAVTAAQST......ISKGENNPGFQNTDDVQTSF 805

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum BB seq length: 0

Maximum Match 100%
Listing first 45 summaries

Database:

PIR_73:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 2 2 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 |) | Result No. |
|--|--------------------|------------------|
| 1344 1334 1334 1334 1313 1310 1310 1310 | 4281 | Score |
| 331. 12. 331. 331 | 99.8 | Query Match L |
| 1306 1306 1313 1313 1313 1313 1313 1313 | 804 | Length DB |
| 11 A3311 A33 | 2 T14 | 3 ID |
| A31755 A31755 A31755 A31655 A3462 JC2038 JC2038 JC2038 JC2038 JC2534 A55472 A55472 A5573 JC5374 A71316 | 1762 | |
| peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida peptidyl-dipeptida angiotensin-conver hypothetical protee hypothetical protee probable thermosta peptide synthetase zinc metalloprotei zinc metall | hypothetical prote | Description |

| 30 119.5 31 119.5 32 119.5 33 118.5 34 117 35 117 36 116 37 116 38 115.5 40 115.5 41 115.4 42 115.4 42 115.4 43 114.5 | |
|---|--|
| 22222222222222222222222222222222222222 | |
| 1283 3655 4540 1780 1780 1642 1575 1642 1933 611 3433 3433 952 952 | |
| +00000 $+$ 0000000000000000000000000000 | |
| \$52500 T38084 T30838 T17272 G95129 G82905 G82905 G82905 T08886 T08881 B97316 B9 | |
| SWH1 protein homol TRAP-like protein cytoplasmic dynein hypothetical prote 1,4-alpha-glucan b conserved hypothet conserved hypothet NMDA receptor-bind probable S-layer p probable S-layer p probable oligoendo utrophin - human thermostable carbo hypothetical prote hypothetical coile phage infection pr hypothetical prote | |

ALIGNMENTS

| 481 | | 4- | 0 |
|------|--|---------------------------------|------------|
| 420 | TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSISAATKAHIASI | Qy 362 Db 361 | p 64 |
| 100 | | b 301 | Db |
| 361 | WDAQRIFKEAEKEFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC | у 302 | Оу |
| 300 | | b 241 | дb |
| 301 | | Y 242 | Qy |
| 240 | |) 181 | ρb |
| 241 | EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH | / 182 | Qy |
| Tao | |) 121 | Db |
| 181 | TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLMAWESWRSEVGKOLRPLYE | , 122 | Qy |
| 12U | MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKKLNTILN | 61 | Дb |
| 121 | | 62 | Qy |
| 60 | | <u> </u> | Db |
| 61 | | 2 | Qy |
| g | | Query Ma Best Loc Matches | |
| | ZP434A014.1 | Note: DKF | P C |
| | A;Cross-Felerences: adult testis; clone DKFZp434A014 A;Experimental source: adult testis; | Cross-re Experime | A . |
| | A; Residues: 1-804 < NANN> A; Residues: 1-804 < NANN> | A; Residues | A; |
| | A;Status: preliminary | Status: | 2 A S |
| | A; Reference number: Z18181 A.Accession: T14762 | Referenc | A A |
| | C;ACCESSIOU: 114,702 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999 | Vambutt, | S R C |
| 1999 | <pre>iens (man) #sequence_revision 20-Sep-1999 #text_change 20-Sep-</pre> | species: Date: 20 | 66 |
| | KESULF 1 T14762 hypothetical protein DKFZp434A014.1 – human (fragment) | T14762 hypothetic | T1. |
| | | | j |

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A; Note: neither the complete nucleic acid sequence nor the complete translation are show C; Comment: For the renal and pulmonary splice form, see PIR:A31759.

A; Gene: GDB:DCP1; ACE
A; Gene: GDB:DCP1; ACE
A; Cross-references: GDB:119840; OMIM:106180
A; Map position: 17q23-17q23
C; Function:
C; Superfamily: mammalian peptidy1-dipeptidase A
C; Superfamily: mammalian peptidy1-dipeptidase A
C; Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidy1dipeptide hyd
E; 22-732/Product: peptidy1 dipeptidase I #status predicted <SIC>
E; 23-732/Product: peptidy1 dipeptidase I #status predicted <MAT>
E; 103,121,140,186,388,617,651/Binding site: zinc, catalytic (His, His, Glu) #status predicted
E; 414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
E; 414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X16295; NID:928264; PIDN:CAA34362.1; PID:928265
R;Ehlers, M.R.W.; Fox, E.A.; Strydom, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A;Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis A;Reference number: A33979; MUID:90046671; pMID:2554286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas FEBS Lett. 252, 99-104, 1989
A.Title: The testicular transcript of the angiotensin I-converting enzyme encodes A.Reference number: S05238; MUID:89338720; PMID:2547653
A.;Accession: S05238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:g338667
A;Experimental source: clones R1.2 and T8B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-732 <EHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man) (c:Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999 C:Accession: S05238; A33979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-732 <LAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidyl-dipeptidase A (EC 3.4.15.1) precursor, testicular splice form - human N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypepti
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                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 SFYGWSTDWSPYADQSIKYRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKYKNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602 SFYGWSTDWSDYADQSIKYRISLKSALGDKAYEWNDNEMYLFRSSYAYAMRQYFLKYKNQ 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 480
TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
                                                                         259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEFLGIQPTLGPPNQPPVSTWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPY 780
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                                                                                         Similarity
                                                       Conservative 119; Mismatches
                                                                                   31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.
                                                                              Score 1344; DB 1;
Pred. No. 8.5e-85;
                                                                                              DB 1; Length 732;
                                                       Indels
                                                    38;
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                                                 10;
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                                         C; Genetics:
                                                                 A; Experimental source: C; Comment: This splice
                                                                                                                                                             A; Accession: PQ0004
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640 LHGEKLGWPQYNWTPNSARS 659
                                                                                                                                                                                                                                   520 RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
                                                             601 --NSFVGW-STDWSPYADQS 617
                                                                                                                                                               541 KCDISNSTEAGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK 600
                                                                                                                                                                                                                                                                                            481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                                                                                                                                             461 LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                                                                                                                                                                                                          421 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 YVRAKIMNAY-PSYISPIGCLPAHLIGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 NNAGDKWSAFLKEQSTLAQMYPLQETQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVELINQAARLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
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R;Soubrier, F;; Alhenc-Gelas, F; Hubert, C.; Allegrini, J;; John, M; Tregear, G.; C Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988 A;Title: Two putative active centers in human angiotensin I-converting enzyme reveale A;Reference number: A31759; MUID:89071703; PMID:2849100 A;Accession: A31759 C; Accession: A31759; PQ0004 C;Species: Homo sapiens (man) C;Date: 07-Jun-1990 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999 peptidyl-dipeptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - hum N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxype

A;Molecule type: mRNA A;Residues: 1-1306 <SOU> A;Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286

A; Experimental source: kidney
A; Note: parts of this sequence, including the amino end of the mature protein, were d
R; Takeuchi, K; Shimizu, T; Ohishi, N; Seyama, Y; Takaku, F; Yotsumoto, H.
J. Biochem. 106, 442-445, 1989
A; Title: Purification of human lung angiotensin-converting enzyme by high-performance

A; Reference number: PQ0004; MUID: 90110025; PMID: 2558109

A;Molecule type: protein A;Residues: 'XX',32-34,'E',36-37,'X',39-41,'R',43-46 <TAK>

A; Gene: GDB: DCP1; ACE Comment: This splice form is found in many tissues, in particular kidney and lung

A; Cross-references: GDB:119840; OMIM:106180

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A; Map position: 17q23-17q23

C; Function:
A; Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti
A; Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti
A; Note: plays a role in the control of blood pressure by catalyzing the conversion of an
C; Superfamily: mammalian peptidyl-dipeptidase A
C; Reywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; me
F; 129, Domain: signal sequence *status predicted <SIG>
F; 30-1306/Product: peptidyl dipeptidase I *status predicted <MAT>
F; 30-1306/Product: peptidyl dipeptidase I *status predicted <TRM>
F; 30-1306/Product: peptidyl dipeptidase I *status predicted <TRM>
F; 30-1306/Product: peptidyl dipeptidase I *status predicted <TRM>
F; 30-394/Binding site: zinc (His) *status predicted
F; 390,394/Binding site: zinc, (His) *status predicted
F; 390,394/Binding site: zinc, catalytic (His, His, Glu) *status predicted
F; 300,734: Cil.** *citation catalytic (His, His, Glu) *status predicted
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                                                                        peptidy1-dipeptidase A (EC 3.4.15.1), testis - mouse
N;Alternate names: peptidy1-dipeptidase I, testis
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35655
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R;Howard, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E. Mol. Cell. Biol. 10, 4294-4302, 1990
A;Title: Transcription of testicular angiotensin-converting enzyme (ACE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT-----
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A;Reference number: A35655; MUID:90318396; PMID:2164636
A;Accession: A35655
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <HOW>
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                                                                                                                                                                                                                                   peptidy1-dipeptidase A (EC 3.4.15.1) precursor - mouse N;Alternate names: ACE; angiotensin-converting enzyme; carboxycathepsin; dipeptidy1 c ()Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A34171; A29220; A61477 R;Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A. J. Biol. Chem. 264, 11945-11951, 1989 A;Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous A;Reference number: A34171; MUID:89308599; PMID:2545691 A;Accession: A34171; MUID:89308599; PMID:2545691
A;Molecule type: mRNA
A;Residues: 1-1312 <BER>
A;Cross-references: GB:J04947
A;Cross-references: GB:J04947
R;Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.; Striker,
J. Biol. Chem. 263, 11021-11024, 1988
A;Title: The isolation of angiotensin-converting enzyme cDNA.
A;Reference number: A29220; MUID:88298730; PMID:2841312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475
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N;Alternate names: angiotensin converting enzyme C;Species: Gallus gallus (chicken)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
C;Accession: JC2489
R;Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
       Biochem. Biophys. Res. Commun. 205
A;Title: Chicken lacks the testis
                                                                                                                                                       peptidyl-dipeptidase A (EC 3.4.15.1) - chicken N;Alternate names: andiotensin convention --
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R;Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.
Kidney Int. 33, 652-655, 1988
A;Title: Partial protein sequence of mouse and bovine kidney angiotensin con A:Reference number: A61477; MUID:88215372; PMID:2835538
A;Excession: A61477
A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-54 < KE33>
C;Superimental source: kidney
C;Superimental source: kidney
C;Superfamily: manmalian peptidyl-dipeptidase A
C;Keywords: alternative spilcing; blood pressure control; membrane protein;
F;1-34/Domain: signal sequence #status predicted <NAT>
F;35-1312/Product: peptidyl dipeptidase I #status predicted <NAT>
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A;Molecule type: mRNA
A;Residues: 1-332 <BE2>
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                                                                                                                                                                                                                                                                                                                                      558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSFVGW-STDWSP 612
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A; Molecule type: mRNA
A; Residues: 1-1193 <EST>
A; Residues: 1-1193 <EST>
A; Cross-references: GB:L40175; NID:g685168; PIDN:AAA75554.1; PID:g994708
A; Cross-references: GB:L40175; NID:g685168; PIDN:AAA75554.1; PID:g994708
C; Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase the c; Superfamily: mammalian peptidyl-dipeptidase A
C; Superfamily: mammalian peptidyl-dipeptide hydrolase; zinc
C; Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc
C; Keywords: metal binding site: zinc, catalytic (Glu, His, Glu, His) #st:
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AVTEFHAATDTADFLGMSVGTKQATAGAW-----VLLALALVFLITSIFLGVK 1175
                                         ADQSIKVRISLKSALG-----DKAYEWNDNEMYLFRSSVAYAMRQYFLKVK
                                                                                       AMKLGFSKPWPEAMQLITGQPNMSAEALMSYFEPLMTWLVKKNTENGEVLGWPEYSWTPY
                                                                                                                                                                                    DFDPGAKFHIPANVPYIRYFVSFVIQFQFHQALCKAAGHTGPLHTCDIYQSKEAGKLLGD
                                                                                                                                                                                                                              YCDPASLFHYSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFN 556
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                                                                                                                                      MLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWL--KDQNKNSFVGW-STDWSPY
                                                                                                                                                                                                                                                                               NYLMSIALDKIAFLPFGYLMDQWRWKVFDGRIKEDEYNQQWWNLRLKYQGLCPPVPRSED
                                                                                                                                                                                                                                                                                                                        NFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDET 496
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                                                                                                                                                                                                                                                                                                                                                                                                                     GHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLIPMPQEFWDKSMIEKPADGREVVCHASAWDFYNRKDFRIKQCTVVNMDDLITVHHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDL-GKGDFRILMCTKVTMDDFLTAHHEM 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAQAKEFLSEYNSTAEVVWNAYTEASWEYNTNITDHNKEVMLEKNLAMSKHTIEYGMRAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264;
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C;Accession: JC2038

R;Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.

Biochem. Biophys. Res. Commun. 198, 380-386, 1994

A;Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs A;Reference number: JC2038; MUID:94121658; PMID:8292044

A;Accession: JC2038

C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

N;Alternate names: angiotensin converting enzyme; kininase II

peptidyl-dipeptidase A (EC 3.4.15.1) - rat

A; Molecule type: m: A; Residues: 1-1313

mRNA

<KOI>

con

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peptidyl-dipeptidase A (EC 3.4.15.1) precursor, testicular - rabbit
N;Alternate names: anglotensin I-converting enzyme; dipeptidyl carboxypeptidase I; pe
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34402; A66724; A36232; C18700
R;Kumar; R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
J. Blol. Chem. 264, 16754-16758, 1989
A;Title: Structure of testicular anglotensin converting enzyme. A segmental mosaic is
A;Reference number: A34402; MUID:89380303; PMID:2550457
A;Accession: A34402
A;Molecule type: mRNA
A;Residues: 1-737 <KUM>
A;Cross-references: GB:J05041; NID:g164744; PIDN:AAA31153.1; PID:g164745
A;Cross-references: GB:J05041; NID:g164744; PIDN:AAA31153.1; PID:g164745
A;Title: Anglotensin-coverting enzyme: structural relationship of the testicular and
A;Reference number: A60724; MUID:91155372; PMID:1705622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U03734; NID:g437289; PIDN:AAA82111.1; PID:g437290
A;Note: the authors translated the codon ACC for residue 159 as Tyr
C;Comment: This enzyme is a zinc-containg dicarboxy peptidase that cleaves angiotensin C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the t C;Superfamily: mammallan peptidyl-dipeptidase A C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; z F;393-400,990-998/Region: catalytic #status predicted
F;1264-1284/Domain: transmembrane #status predicted <TMM>
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A;Accession: A60724
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 73-173 (SEN)
A;Note: identical sequences were obtained for mRNAs from lung and tR;Chen, Y.N.P.; Riordan, J.F.
Biochemistry 29, 10498-10498, 1990
A;Title: Identification of essential tyrosine and lysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 33-35,'SN',38-39,'SS';'FAEL',737 <IWA>
A;Residues: 33-35,'SN',38-39,'SS';'FAEL',737 <IWA>
A;Note: several of the amino acids in reported are tentative
C;Comment: The pulmonary and testicular isoforms of this enzyme differ substantially
C;Comment: The pulmonary and testicular isoforms of this enzyme differ substantially
G;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; testis; transmembrane
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A; Residues: 154-160; 236-242 < CHE>
A; Residues: 154-160; 236-242 < CHE>
R; Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
B; Title: The NH2-and COOH-terminal sequences of the angiotensin-converting
A; Reference number: A90107; MUID:83048249; PMID:6291514
A; Accession: C18700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                 CPPAPRSQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS
                                                                                                                                                                                                                                                                  VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIRPLYEHLHAYVRAKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANVCRVDG--SCLQLEPDLTNLMATSRKYDELLWVWTSWRDKVGRAILPYFPKYVEFTNK
WPOYTWTPNSARS
                                                      W-STDWSPYADQS 617
                                                                                                                  KEAGKRLADAMKLGYSKPWPEAMKVITGQPNMSASAMMNYFKPLMDWLLTENGRHGEKLG
                                                                                                                                                                  TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
                                                                                                                                                                                                                                                                                                                                                                                                    FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLVVVHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSINLLSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEADKFF ISLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAY-PSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE
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                                                                                                                                                                                                                                                                                                                                                 -GGGYEHDINFLMKMALDKIAFIPFSYLVDEWRWRVFDGSITKENYNQEWWSLRLKYQGL
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   664
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A; Restruct.
A; Cross-references: GB:M585/y
A; Cross-references: GB:M585/y
R; Ramchandran, R.; Sen, G.C.; Misono, K.; Sen, I.
R; Ramchandran, R.; Sen, G.C.; Misono, K.; Sen, I.
J. Biol. Chem. 269, 2125-2130, 1994
A; Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting
A; Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting
A; Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 34-55 <KIR>
C;Comment: This enzyme converts angiotensin I to angiotensin II in presence of ver, the enzyme has been found also in renal tubules and intestinal mucosa.
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; blood pressure control; chloride; glycoproteins, chloride; glycoproteins, control; chloride; chloride
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35484; A23455, A18700; A38655; A49726; S17509
R;Thekkumkara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.
Nucleic Acids Res. 20, 683-687, 1992
A;Title: Use of alternative polyadenylation sites for tissue-specific transcription
A;Reference number: S35484; MUID:92178960; PMID:1311831
                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule A; Reference number: S17509; MUID:91378880; PMID:1654880 A; Accession: S17509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
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Biochem. J. 278,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1236-1258 < RAM>
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A; Residues: 1-88 < KUM>
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A;Residues: 34-44;754-755,'L',757 <IW2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1309 <THE>
A; Cross-references: EMBL: X62551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit N.Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: testis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-33/Domain: signal sequence #status predicted <SIG>
34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental
39,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (
                                                                                                               647
                   70
                                                                                                                                                                                                                                                                                                                                                   POCGI
         SAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST
                                                                                                 TDEAEASRFVEEYDRSFQAVWNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNW
                                                                                                                                                                                                  TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----
                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                         29.9%;
                                                                                                                                                                                                                                                                                                                                     Score 1283; DB 1;
Pred. No. 3.4e-80;
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                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                  -NVQNMNN--AGDKW 69
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                                                                                                                                                                                                                                                                                              38;
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Matches

Local Similarity

Conservative

108; Pred.

Mismatches 246; No.

Indels

22;

Gaps

7;

3.8e-65;

8 LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD

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Eur. J. Blochem. 237, 414-423, 1966

A;Title: Cloning and characterisation of angiotensin-converting enzyme from A;Reference number: $65472

A;Reference number: $65431; MUID:96215437; PMID:8647080

A;Accession: $65472

A;Molecule type: DNA

A;Molecule type: DNA

A;Cross-references: EMBL:L43965; NID:9908759; PIDN:AAA70427.1; PID:9908760

A;Mote: the source is designated as Haematobia irritans exigua

A;Accession: $65431

A;Molecule type: protein

A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Residues: 18, 'P'
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N;Alternate names: angiotensin I-converting enzyme
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Accession: S65472; S65431
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.;
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24.7%;
                               Score 1058;
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peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster N;Alternate names: angiotensin-converting enzyme C;Species: Drosophila melanogaster C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998 C;Accession: A57533
C;Accession: A57533
A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin A;Reference number: A57533; MUID:95293950; PMID:7775412
A;Accession: A5753
A;Residues: 1-615 CCOR>
A;Cross-references: GB:U25344
C;Genetics:
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C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: peptidyldipeptide hydrolase
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                83
                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIED-VEHTFEEIKPLYEHLHAYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKVRVCDYKNSAKCDLSLDPEIEEIITKSRDPEELKYYWTQFYDKAGTPTRSNFEKYVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTKSAKLNNFTDGAEVWLDEYE------DATFEDQLEAIFEDIKPLYDQVHGYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENAKFLKEVAKDIQKFNWRTYGSADVRRQFKSLSKTGYSALPAEDYAELLEVLSAMESNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLDNCDIYGSKEAGKLFENMLSLGASKPWPDALEAFNGERTMTGKAIAEYFEPLRVWLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAA-----KHEG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKRE 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTQDQFFTVHHEMGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLERVGL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKMFQMGDDFFQSMGLKKLPQEFWDKSILEKPDDGRDLVCHASAWDFYLTDDVRIKQCTR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRLNKFYGDEVVSKTGPLPMHLLGNMWAQQWSSIADIVSPFPEKPLVDVSDEMVAQGYTP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILAGLAVCHGATKEEIVATEYLQNINKELAKHTNVETEVSWAYASNITDENERLRNEISA
                                         KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRYLVSFIIQFQFYKSACITAGEYVPNQTEY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LK-NYVSDNEARINQLFLTALDKIVFLPFAFTMDKYRWALFRGQADKSEWNCAFWKLREE 475
                ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF
                                                                                                                                              LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD
                                                                                                    LLATLAVTQALVKEEIQAKEYLENLNKELAKRTNVETEAAWAYGSNITDENEKKKNEISA 67
                                                                                                                                                                                            Conservative
                                                                                                                                                                                          24.2%; Score 1039; I
35.8%; Pred. No. 7.86
tive 120; Mismatches
                                                                                                                                                                                          7.8e-64;
nes 251;
                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                      Length 615;
                                                                                                                                                                                            Indels
                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Acer
C;Superfamily: mammalian peptidyl-dipeptidase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X96913; NID:g1405881; PIDN:CAA65632.1; PID:g1405882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Taylor, C.A.M.; Coates, D.; Shirras, A.D. Gene 181, 191-197, 1996
A;Title: The Acer gene of Drosophila codes A;Reference number: JC5374; MUID:97128790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-630 <TAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC5374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                               Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
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                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                       75
                                                                                                                                                                                                                                         16 WLPHGLSMGNSCSASVLE-ARRFFELENEQLRRRFHEEFLSGYNYNTNVTEANRQAMIEV
                                                                                                                                                                                                                                                                                6 WILLSIVAYTAAQSTIEEQAKTFIDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTKAAKLNNFTSGAEAWLDEYE-----DDTFEQQLEDI---FADIRPLLPADPWLCAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKVKVCDYKDSTKCDLALDPEIEEVISKSRDHEELAYYWREFYDKAGTAVRSQFERYVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-DYVRDDEARINQLELTALDKIVELPFAFTMDKYRWSLERGEVDKANWNCAFWKLRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIFKEAEKFFYSYGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLRKHYGDAVVSETGPIPMHLLGNMWAQQWSEIADIVSPFPEKPLVDVSAEMEKQAYTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIKNNVHIGWTT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N--KNSFVGWST 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDNCDIYGSARAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQ 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGIEPPVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP
                                                                                                    IYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYV 184
                  VLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYV
                                                              NYATATYCSYTNRSDCSLTLEPHIQERLSHSRDPAELAWYWREWHDKSGTPMRQNFAEYV 194
                                                                                                                                                     YARNAELNKRLAQQIKSSDYVQSEDADIRRQAEHLSKLGASALNADDYLALQNAISSMQT
                                                                                                                                                                                            GDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMST
                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                   Conservative 113; Mismatches
                                                                                                                                                                                                                                                                                                                                                      24.0%; Score 1030; DB 2; 35.6%; Pred. No. 3.4e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for an angiotensin-converting enzyme homo PMID:8973330
                                                                                                                                                                                                                                                                                                                                                                                Length 630;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                        24;
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715792
715792
hypothetical protein C42D8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15792
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A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8
A;Reference number: Z18405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                             337 NIITISNEGAKLNGFANGGAMWRSAFDMSSKVHKAEF---DLNKQIDKIYSTIQPFYQLL
241 HAYVRAKLMNAY--PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMV 298
                                                                                                                                         278 ALNRDSKDSTICDKDVPPPCALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYN
                                                                                                                                                                                     122 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                218 LDEAENVLTMFVRSTSMQAKQFDMASVTDEKVMRQLGYVSFEGMSALAPSRFADYSQAQA 277
                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 LTLDNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEEFTGETEMDPAALLEYFEPLYQWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 DQNKNSFVGWSTDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 VQKLFELGDQFFQSLGMRALPPSFWNLSVLTRPDD-RQVVCHASAWDFYQDSDVRIKMCT
                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                         EYVVLKNEMARANHYEDYGDYWRGDYEVNG-VDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                                                                                                                                                                                            SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA 217
                                                                                                                                                                                                                                                                                                                                                                        SSSSWILLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN 61
                                                                                                                                                                                                                                                                                 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QE--NSRLGVPLGWGP 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      efggveppvfrtekdfdppakyhidadveylryfaahifqfqfhkvlcrkagqyapnnsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFRLRQHYGPDVMPAEGNIPISLLGNMWGQSWNELLDLFTPYPEKPFVDVKAEMEKQGYT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLTRKASQLNGHRSYADYWVQFYE-----DPDFER-----QLDATFKQLLPLYRQLHGYV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LHKCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVDSHYFYVVHHELGHIQYYLQYEQQPAVYRGAPNPGFHEAVGDVIALSVMSAKHLKAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIE-NGRLDEKSRINQLFKQALSKIVFLPFGYAVDKYRYAVFRNELDESQWNCGFWQMRS 482
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 642.5; DB 2; 27.0%; Pred. No. 3.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 907;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 41;
                                                  393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602
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                   Ωy
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83696
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
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A; Gene: BH(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA A;Residues: 1-532 <STO>
A;Residues: 1-532 <STO>
A;Cross-references: GB:AP001508; GB:BA0000004; NID:g10172890; PIDN:BAB04090.1; GSPDB:GA;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
         297 MYDQAWDAQRIFKEAEKFFYSYGLPNWTQGFWENSMLTDPGNYQK-AYCHPTAWDLGKGD 355
                                                       212 KDEIDEERAKVLKIKKDDLRP------250
                                                                                                                                                                                               188 NEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHT----FEEIKPLYEHLHAYV 244
                                                                                                                                                                                                                                             119 NGSRVSNNE------LLDTLRYDLDHERRKQAWFA-SKEVGKRTEKDLLQLIRKR 166
                                                                                                                                                             167 NEVARNLGFETF-
                                                                                                                                                                                                                                                                                           128 STGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           631 KLNDRWWEIRNKYEGVRSPQPYNTSNLD--ALIHNSVSQVHS----PATRTLISYVLKFQI 685
                                                                                                                                                                                                                                                                                                                                    63 VTRFRKIDSLPLMQRRQLDDLHDKMIKNQFE--EGTRQQILSLE--KKISHVFTTFQPQV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 PLLNYFEPLFTWLKDQNK--NSFVGWSTDWSPYADQSI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 LKALCQRELFWLSEG----CILSEDTT--EKLRETMKLGSSITWLKALEMISGKGELDAQ 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 PNDFRVKACAQLGEPDFEQAHSLLVQTYYQYLYKDQSLLFREQASPVITDAIANAFAHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-NVQNMNNAGDKWSAFLKEQS--- 77
                                                                                                                                                                                                                                                                                                                                                                                                                             3 EQDIERFLSEQNKRVEDLYQPVLLNHWMVATTGEQEWSDKHEQSLSEYWAHFSDRESFQK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH0371
                                                                                                     -----RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQK-PNIDVTDA 296
                                                                                                                                                                                                                                                                                                                                                                                    -----TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEALCQAA---KHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVR 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH--VSNDYSFIRYYTRTL----YQFQF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPKHLKSIGLLSPDFQEDNETE-INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKD 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLEYYEPLINWLRNTNEIDQVVVGWDGEGTPFTVEEI 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNPHYLYSQKLVPSEHLDIKDSVIINKLYKESLESFTKLPFTIAADNWRYELFDGTVPKN 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAFNTQNYTTKKMEVTAYRYEKSAGEPHLPKSYWTSSIFARVWS-KDMICHPAAALDMRA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D----QAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHP-TAWDL-G 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 157; DB 2;
Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 213; Indels 144;
                                                                                                                                                     YHMSFATQELDLEQTFAMFETIKKSSDQAFRMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 532;
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Gaps

| Qy 178 PLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGY DYSRGQLIEDVEHTFEEIKP 235 | 28 128; CONSERVATIVE 20 TIEEQAKTFLDKFNHEAEDLF - | AF1310 probable thermostable carboxypeptidases homolog lmo1886 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27.Nov-2001 #sequence_revision 27.Nov-2001 #text_change 14.Dec-2001 C;Accession: AF1310 R;Glaser, P: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Status: preliminary A;Molecule type: DNA A;Residues; 1-502 <gla> A;Cross-references: GB:NC_003210; PIDN:CAC99964.1; PID:g16411339; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics: A;Gene: Lmo1886 C;Superfamily: Thermus aquaticus carboxypeptidase Taq Query Match Best Local Similarity 20.1%; Pred. No. 0.0086;</gla> | Db 251 -FDSFYKDQDLEQVVSQTFQAMELPIDDILKRSDLYPRKNKNPFGFCTDMD-RRGD 304 Qy 356 FRILMCTKVTMDDFLTAHHEMGH-IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAAT 414 |
|--|---|--|--|
| QY 180 YEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLY 237 | 124; CONSETVA | RESULT 16 AE1682 AE1682 probable thermostable carboxypeptidases homolog lin1999 [imported] - Listeria innocua C;Species: Listeria innocua C;Dectes: Cisteria innocua C;Date: 27 Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AE1682 R;Glaser, P:, Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Cross-references: GB:AL592022; PIDN:CAC97229.1; PID:g16414500; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;Genetics: A;Gene: lin1999 C;Superfamily: Thermus aquaticus carboxypeptidase Taq Query Match 3.48; Score 147; DB 2; Length 502; Best Local Similarity 19.48; Pred. No. 0.026; | Db 244 VRITTRYNENDFKMAVFGTIHEGGHAIYEQNEDAALVGTPLANGASMGIHESQSLF 299 406 -EIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLP- 451 |

| Qγ | рb | Db Qy | Оy | ОУ | Qу Db | Db Qy | Оу | Que Bes Ma | A;Referen A;Accessi A;Status; A;Molecul A;Residue A;Cross-r A;Experim C;Genetic A;Gene: a | R; Kai Naki DNA 1 A; T1 | RESULT AI2011 peptid C; Spec A; Note C; Date C; Acce | Оy | Qy Db | ОУ | Ωу | Ü |
|--|--|---|---|--|--|---|--|---|---|--|--|---|---|--|--|--|
| 425 | 365 419 | 319 360 | 275 305 | 218 269 | 158 220 | 112 160 | 52 106 | Query Ma Best Loc Matches | Reference Accession Status: po Molecule Residues: Cross-ref Experimen Genetics: | neko, azaki, Res. E tle: C | LT 17 11 11 ide sy ecies: ecies: te: No te: 14 cessic | 563 466 | 507 410 | 451 356 | 302 | 246 |
| SPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484 | TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGIL 424 : : : : | GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKV 364 : | WTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV- 318 | SRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRF 274 : : :: | YNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDY 217 :: : ; ; ; ; ; ; ; ; | KSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLD 157 : : : : | TNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSED 111 | / Match 3.3%; Score 139.5; DB 2; Length 987; Local Similarity 19.6%; Pred. No. 0.24; nes 117; Conservative 80; Mismatches 208; Indels 191; Gaps 26; | <pre>n number: AB1807; MUID:21595285; PMID:11759840 n: AI2011 preliminary preliminary type: DNA type: DNA type: CNR type: CNR type: CNR type: CNR type: CNR type: DNA type: CNR type: CNR type: DNA type: DNA</pre> | , T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch i, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, 8, 205-213, 2001 Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An | nc sp. (strain PCC 7120) a synonym of Anabaena sp. strain PCC n 14-Dec-2001 #text_change 30-Jun-2002 | SEPWILALENVYGAKNMNVRPLLNYFEPLFTWLKDQNK 600 :: | SNDYSFIRYYTRTL-YQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGK 562 | PFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHV 506 | VGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTL 450 IIIGSSLAFWKSNYADFQAITKPAFDHVKLEDFYRAVNISESSLIRIBADTLTY 355 | ITTRYNENDFKMAVFGTIHEGGHAIYEQNFDAALVGTPLANGASMGIHESQSLFYE 301 |

| Qy 535 HEGPLHKCDI-SNSTEAGQKLENMLRLGKS-EPWTLALENVVGAKNMNVRPLLNYFEPLF 592 | Db 485 AYLEINHDYTGYKYNKNKISKYDEANALILINIPHFYTGNFYVYKYVIGQIC 536 | Qy 487 VVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQ-EALCQAAK 534 | Qy 428 FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWAVFKGEIPKDQWMKKWWEMK-REIVG 486 : : : : : : : : : Db 432 YENDDLMRLYILDEMISGFIATTTRQAIFSNFEWVANEWINQGEEFSWNKIVL 484 | | Qy 308 FKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMD 367 | Qy 249 MNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVDFGQKPNIDVTDAM-VDQAWDAQRI 307 | Qy 191 ARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEBIKPLYEHLHAYVRAKL 248 : :::: : : : :::: | Qy 131 KVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEM 190 | Qy 95YSTG 130 125 LIKYQLEYEBLWRYEKHILNEQQQKVVTAISRFSSSFGDIFDVLLDSDMQYQDGINYKKQ 184 | OY 49 NYNTNITEENVQNMNNAGDKWSAFLK-EQSTLAQMYPLQEIQNLTVK94 | Query Match 3.2%; Score 136; DB 2; Length 611; Best Local Similarity 19.5%; Pred. No. 0.2; Matches 119; Conservative 100; Mismatches 256; Indels 134; Gaps 27; | C;Generics: A;Gene: pepF-2; UU521 A;Genetic code: SGC3 | | .; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. GenBank, February 2000 n: The complete sequence of Ureaplasma urealyticum: Alternate views of a number: A82870 | INAZURI zinc metalloproteinase oligoendopeptidase F UU521 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: D82881 | Qy 567 TLALENVVGAKNMNVRPLLNYFEPLFTWLKD 597 | Qy 524 QFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPW 566 1 | Db 486 LELEYTNKPIVEDLNSIYSLSSITPLRIPHFYVGNEYVYKY 526 |
|---|--|---|---|--|---|---|--|---|---|--|--|---|---|--|--|--|---|--|
| QY 540 HKCDISNSTEAGQKLFNMLRL-GKSEPWTLALENVVGAKNMNVRPLLNY 587 | Db 394 ITPQTDAEGILQDVHWAGGDFGYFPSYALGYMYAAQLKQKMLEDLPEFDALLERGEF 450 | QY 487 VVEPVPHDETYCDPASLFHVSNDYS-FIRYYTRTLYQFQFQEALCQAAKHEGPL 539 | Qy 429 QEDNETEINFLIKQALTIVGTLPFTYMLEKWRMMVFKGEIPKDQWMKKWWEMKREIVG 486 : : : : : : : : | AAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDF- | QY 332 MLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHEMGHIQYDMAY 385 | QY 279 YSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFEVSVGLPNMTQGFWENS 331 | Qy 219 RGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNL 278 | Qy 180 YEEYYVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYS 218 | Query Match 3.1%; Score 135; DB 2; Length 501; Best Local Similarity 20.9%; Pred. No. 0.18; Matches 98; Conservative 65; Mismatches 164; Indels 142; Gaps 26; | C;Genetics: A;Gene: ypwA C;Superfamily: Thermus aquaticus carboxypeptidase Taq | A; Notecute type: DNA A; Molecule type: DNA A; Residues: 1-501 <kun> A; CB: A: A: CB: A: A: CB: A: A</kun> | A;IILLE: IHE complete genome sequence of the stam posterior bacterian business. A;Reference number: A69580; MUID:98044033; PMID:9384377 A;Accession: D69943 A.Gratus. proliminary: pugleic acid sequence not shown: translation not shown | y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya akeuchi, M.; Tamakoshi, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. | A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Larding A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Malizzi, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A;Authors: Lauber, A; | R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997 | RESULT 20 D69943 carboxypeptidase homolog ypwA - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Bace: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 | Qy 593 -TWLKDQNK 600 | Db 537GLINAIRIFNNKANAKEKYFCFFKSGGSLSPLETINILDIK-INENDVWEEVNIIF 591 |

В 451 HPIK-----QWLTEKVHIHGKRKKPLDIIKDATG-EELNVRYLIDY 490

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"Angiotensin-converting enzyme: zinc- and inhibitor-binding stoichiometries of the somatic and testis isozymes."; Biochemistry 30:7118-7126(1991).
                                                                                                       Ehlers M.R., Riordan J.F.
                                                                                                                          MEDLINE=91308093; PubMed=1649623;
                                                                                                                                                                                                                                                                                                                                            MEDLINE=90110025; PubMed=2558109;
Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
                                                                                                                                                                                                                                                                                   "Purification of human lung angiotensin-converting enzyme by high-
                                                                                                                                                                               ZINC-BINDING
                                                                                                                                                                                                                                                             performance liquid chromatography: properties and N-terminal amino
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.; "Sequence variation in the human angiotensin converting enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE OF 30-46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS S-261; W-561 AND S-1286. MEDLINE=99251580; PubMed=10319862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          revealed
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01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
CACE) (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two putative active centers in human angiotensin I-converting enzyme revealed by molecular cloning";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soubrier F., Alhenc-Gelas F., Hubert C., Allegrini J., John M.,
Tregear G., Corbol P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89071703; PubMed=2849100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                CARBOHYD
CARBOHYD
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METAL
ACT_SITE
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ACT_SITE
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PIR; PQ0004; PQ0004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04144; AAA51684.1; -.
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InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            proDom; pD004184; Peptidase_M2; 2.
proSITE; PS00142; ZINC_PROTEASE; 2
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                        CARBOHYD
                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRADYKININ, A POTENT VASODILATATOR.

CATALTYTC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-[-xaa-xbb, when xaa is not Pro, and Xbb is neither algopeptide-[-xaa-xbb, when xaa is not Pro, and Xbb is neither asp nor Glu. Converts angiotensin I to angiotensin II. COTACTOR: BINDS 2 ZINC IONS.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; somatic (shown here) and testis-specific (AC P22966); are produced by alternative splicing. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.

DATABASE: NAME-PROW; NOTE-CD guide CD143 entry; WWW-"http://www.nobi.nlm.nih.gov/prow/cd/cd143.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF118569; AAD28560.1;
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391
394
988
989
992
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ZINC 2 (CATALYTIC)
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                         N-LINKED
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 /FTId=VAR_011707
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INC 2 (CATALYTIC) (BY
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oll-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel

ACET_MOUSE

STANDARD;

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

Chordata; Craniata; Vertebrata; Euteleostomi Rodentia; Sciurognathi; Muridae; Murinae; Mus

SEQUENCE FROM N.A NCBI_TaxID=10090;

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SORFITT
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MOUSE
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                                                                                                                                                                                                                                                                                                                                           LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                                                                                                                                                          ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
                                                             QYNWTPNSARS 1233
                                                                                         STDWSPYADQS 617
                                                                                                                      AGORLATAMKLGFSRPWPEAMOLITGOPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222
                                                                                                                                                    AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 606
                                                                                                                                                                                   PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE
                                                                                                                                                                                                                 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
                                                                                                                                                                                                                                                                              EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Pred. No. 9.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_011708
R -> S.
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D -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ACT_SITE
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PRODOM; PD004184; Peptidase_M2; 1
PROSITE; PS00142; ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:87874; Ace.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                              129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01401; Peptidase_M2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A35655; A35655.
MEROPS; M02.004; -.
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-i- ALTERNATIVE PRODUCTS: 2 isoforms; testis-specific (shown here)
somatic (AC poly470); are produced by alternative splicing.
-i- TISSUE SPECIFICITY: SPERMATOCYTES, ADULT TESTIS.
-i- IDDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M61094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M55333; AAA37149.1; -.
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                                                                                                                                                                                                                                                                 20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ycoprotein;
                                                                                                                                                                                                                                                                                                                                                                            Local
ECLLLEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                           AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG--
                                                                                                                                                AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                       TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128
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CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-xaa-xbb, when xaa is not Pro, and Xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II.

COPACTOR: BINDS 1 ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGULATION BY ANDROGENS
                                                                                                                                                                                                                                                                                                                                                 255;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.-Y., Langford K.G., Martin B.M.,
                                                                                                                                                                                                                                                                                                                                                                      31.1%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84047 MW;
                                                                                                                                                                                                                                                                                                                                           112;
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N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                               Score 1334;
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                                                                                                                                                                                                                                                                                                                                    Mismatches
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NC (CATALYTIC) (BY SIMILARITY).

LINKED (GLCNAC...) (POTENTIAL).

LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                6.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Length 732;
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enzyme (ACE) is
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                                                         THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

-!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-xaa-xbb, when Xaa is not Pro, and Xbb is nei Asp nor Glu. Converts angiotensin I to angiotensin II.
-!- COPACTOR: BINDS 2 ZINC IONS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; somatic (shown here) and specific (AC P22967); are produced by alternative splicing.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                           "The isolation of angiotensin-converting enzyme cDNA.";
J. Biol. Chem. 263:11021-11024(1988).
-i- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anglotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
(ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
                                                                                                                                                                                                                                                                                                                                     Striker G
                                                                                                                                                                                                                                                                                                                                             Bernstein K., Martin B.M., Bernstein E.A., Linton J., Striker
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-332 FROM N.A., AND PARTIAL SEQUENCE MEDILINE-88298730; Pubmed-2841312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernstein K.E., Martin B.M., Edwards A.S., Bernstein E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89308599; PubMed=2545691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P09470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mouse angiotensin-converting enzyme is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                264:11945-11951(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a protein composed of two
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                   a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercement is not removed.
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VARIANT
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CARBOHYD
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ACT_SITE
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
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                                                                                                                                                                                                Local
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A34171; A34171.
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IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
                                       GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP
                                                                                 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                                     AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG--
                                                                                                                       AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                   GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL
                                                             TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA
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M02.004; -.
                                                                                                                                                                                                Similarity
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in; Transmembrane; Repeat; Signal; Alternative splicing.
                                                                                                                                                                                       Conservative
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ALSE Sequence update)
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-1996 (Rel. 39, Last annotation update)
Angiotensin-converting enzyme (EC 3.4.15.1) (I
Carphoxypeptidase I) (Kininase II) (Fragment).
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1056
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                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme found in mammals."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Chicken lacks the testis specific isozyme of angiotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Esther C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95110342; PubMed=7811282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                                      MEROPS; M02.004;
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                                                                                                                                                                                                                                                                                                                                   FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF T VASCOCOMSTRICTOR ACTIVITY OF ANGIOTENSIN.

CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-'-Xaa-xbb, when xaa is not Pro, and xbb i Asp nor Glu. Converts angiotensin I to angiotensin II. COPACTOR: BINDS 2 ZICC IONS.
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.

Prodom; PD004184; PROSITE; PS00142;

Peptidase_M2; 2. ZINC_PROTEASE; 2 ZINC_PROTEASE;

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ADQSIKVRISLKSALG-----DKAYEWNDNEMYLFRSSVAYAMRQYFLKVK
                                               AMKLGFSKPWPEAMQLITGQPNMSAEALMSYFEPLMTWLVKKNTENGEVLGWPEYSWTPY
                                                                                       MLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWL--KDQNKNSFVGW-STDWSPY
                                                                                                                                   DFDPGAKFHIPANVPYIRYFVSFVIQFQFHQALCKAAGHTGPLHTCDIYQSKEAGKLLGD
                                                                                                                                                                YCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFN
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                                                                                                                                                                                                                          NYLMSIALDKIAFLPFGYLMDQWRWKVFDGRIKEDEYNQQWWNLRLKYQGLCPPVPRSED
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(BY
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                                                                                                                                                                                                                                  InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY THE TERMINAL HIS-LEU, THAIS RESULTS IN AN INCREASE OF TVASCOONSTRICTOR ACTIVITY OF ANGIOTENSIN.

-I- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-xaa-xbb, when Xaa is not Pro, and Xbb i ASP nor Glu. Converts angiotensin I to angiotensin II.

-I- COFACTOR: BINDS 2 ZINC IONS (BY SIMILARITY)

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- ALTERNATIVE PRODUCTS: 2 isoforms; somatic (shown here)
  TRANSMEM
                              DOMAIN
                                                                                                          SIGNAL
                                                                                                                                                                              Prodom; PD004184; Peptidase_M2; 2. PROSITE; PS00142; ZINC_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                          MEROPS; M02.001;
MEROPS; M02.004;
                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACE_RAT STANDARD; PRT; 1313 AA. P47820; PRT88-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Angiotensin-converting enzyme, somatic isoform precursor (EC
                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-LEW/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1128 AVTEFHAATDTADFLGMSVGTKQATAGAW-----VLLALALVFLITSIFLGVK 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a missense mutation in the angiotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corvol P., Sternberg E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jafarian-Tehrani M., Listwak S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-converting enzyme cDNA in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koike G., Krieger J.E., Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94121658;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Angiotensin converting enzyme and genetic hypertension: cloning rat cDNAs and characterization of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                ycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific; are produced by alternative splicing. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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                                                                                                                                                                                                                                                                                                                                                                                           AF201332; AAG35597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed.
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  1266
                                                                                                                                              Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
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POTENTIAL
                     EXTRACELLULAR
                                                                                                                             Repeat;
                                                                         ANGIOTENSIN-CONVERTING ENZYME,
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.J., Mukoyama M.,
                                                                                                     peat; Signal; Alternative splicing
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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                                                      LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP
                                                                                            CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM
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                                                                          FDPGSKFHVPANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADA
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Iwata K., Blacher R., Soffer R.L., Lai C.Y.;
"Rabbit pulmonary angiotensin-converting enzyme: the NH2-terminal fragment with enzymatic activity and its formation from the native enzyme by NH4OH treatment.";
Arch. Biochem. Blophys. 227:188-201(1983).
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumar R.S., Thekkumkara T.J., Sen G.C.;
"The mRNAs encoding the two angiotensin-converting isozymes transcribed from the same gene by a tissue-specific choice (alternative transcription initiation sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
                                                                                                                                                  EMBL;
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MEDLINE=84051289;
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MEDLINE=92178960;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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P12822; 002852;
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                                                                                                                                                                                                                                                                                                                            VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, clipopeptide-| raa-xbb, when xaa is not Pro, and Xbb is Asp nor Glu. Converts angiotensin I to angiotensin II.

COFACTOR: BINDS 2 ZINC IONS (BY SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protein.

ALITERNATIVE PRODUCTS: 2 isoforms; somatic (shown here) a specific (AC P22968); are produced by alternative splici SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yme by NH4OH treatment, h. Biochem. Biophys. 227:188-201(1983).
h. Biochem. Biophys. 227:188-201 TO ANGIOTENSIN II BY FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY FUNCTION: GIVE-T.FII. THIS RESULTS IN AN INCREASE OF T
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S35484; S35484.
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M58579; AAA31151.1;
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                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.

PD004184; Peptidase_M2;

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                                  SGRTPSSRYNFDWWYLRTKYQGICPPVVRNETHFDAGAKFHIPSVTPYIRYFVSFVLQFQ
                                               KGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQ
                                                                            GDVLALSVSTPAHLHKIGLLD-HVTNDTESDINYLLKMALEKIAFLPFGYLVDQWRWGVF
                                                                                                GEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVF
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P22968;
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P22968;
P23968;
P2406-1991 (Rel. 19, Created)
P2507 (Rel. 14, Last sequence update)
P2507 (Rel. 41, Last annotation update)
P2507 (Rel. 41, Last sequence update)
P2508 (Rel. 19, Comparison update)
P2508 (Rel. 19, Comparison update)
P2508 (Rel. 19, Comparison update)
P2508 (Rel. 19, Created)
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                                                                          EMBL; J05041; AAA31153.1;
EMBL; M58580; AAA31152.1;
PIR; A34402; A34402.
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entities requires a license
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J. Biol. Chem. 266:3854-3862(1991).

- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RETHE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=New Zealand white; TISSUE=Testis; MEDLINE=89380303; PubMed=2550457; Kumar R.S., Kusari J., Roy S.N., Soffer R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                            entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kumar R.S., Thekkumkara T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91139683; PubMed=1847388;
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Mammalia; Eutheria; Lagomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-xaa-xbb, when Xaa is not Pro, and Xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II. COFACTOR: BINDS 1 ZINC ION.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; testis-specific (shown here) somatic (AC P12822); are produced by alternative splicing.

TISSUE SPECIFICITY: SPERMATOCYTES, ADULT TESTIS.
                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. There by non-profit institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: EXPRESSION IS THOUGHT REGULATION BY ANDROGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHQALCMEAGHQGPLHQCDIYQSTRAGAKLRAVLQAGCSRPWQEVLKDMVASDALDAQPL
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Best Local
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000130; Zn_MTpeptds
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ARRFDVSNFQNATSKRIIKKVQDLQRAVLPVKELEEYNQILLDMETIYSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDEAEASRFVEEYDRSFQAVWNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNN--AGDKW 69
                                                                                                                                                                                                                                           DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
                                                                                                                                                                                                                                                                                                KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMD
                                                                                                                                                                                                                                                                                                                             RHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVAPFPSASTMDATEAMIKQGWTPRRMF
                                                                                                                                                                                                                                                                                                                                                       NAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIF
                                                                                                                                                                                                                                                                                                                                                                                  AARLNGYVDAGDSWRSMYETPTLE------QDLERLFQELQPLYLNLHAYVGRALH
WPQYTWTPNSARS 664
                                                                             TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
                                                                                                         CPPAPRSQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS
                                                                                                                                                                                       FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV
                                                                                                                                                                                                                    DLVVVHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSINLLSSE
                                                                                                                                                                                                                                                                         EEADKFFISLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNME
                        W-STDWSPYADQS 617
                                                   KEAGKRLADAMKLGYSKPWPEAMKVITGQPNMSASAMMNYFKPLMDWLLTENGRHGEKLG
                                                                                                                                VEPVPHDETYCDPASLEHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                              -GGGYEHDINFLMKMALDKIAFIPFSYLVDEWRWRVFDGSITKENYNQEWWSLRLKYQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1283;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGIOTENSIN-CONVERTING ENZYME, TESTIS-SPECIFIC ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FC43CC76655C3DCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6e-82;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACE_DROME STANDARD; PRT; 615 AA.
Q10714; Q27572;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carboxypeptidase ANCE OR RACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin-converting enzyme precursor carboxypeptidase I) (Kininase II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96028519; PubMed=7547464;
Tatei K., Cai H., Ip Y.T., Levine M.;
"Race: a Drosophila homologue of the angiotensin converting enzyme.";
Mech. Dev. 51:157-168(1995).
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornell M.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                ACT_SITE
                                                                                   CHAIN
                                                                                                                                                                                                       InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                          EMBL; U25344; AAB02171.1; -. EMBL; U34599; AAC46902.1; -.
                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                      ProDom; PD004184; Peptidase_M2; 1. PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                         FlyBase; FBgn0012037; Ance
CARBOHYD
                                                                                                                                                                                        PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                          MEROPS; M02.003;
                  CARBOHYD
                                                                    METAL
                                                                                                       SIGNAL
                                                                                                                     Glycoprotein;
                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-{-xaa-xbb, when xaa is not Pro, and xbb i Asp nor Glu. Converts angiotensin I to angiotensin II. COPACTOR: BINDS 1 ZINC ION.
SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: MAY PLAY A ROLE IN THE CONTRACTIONS OF THE HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: EXPRESSED IN THE AMNIOSEROSA DURING GERM BAND ELONGATION, SHORTENING AND HEART MORPHOGENESIS. EXPRESSED IN MIDGUT THROUGHOUT EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND TESTES.
                                                                                                                                         Metalloprotease;
 18
367
368
371
53
196
                                                                                                                     Signal
                                                                                                                                       Carboxypeptidase; Zinc; Dipeptidase;
ZINC (CATALYTIC) (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (POTENTIAL
N-LINKED (GLCNAC. . .) (POTENTIAL
                                                  ANGIOTENSIN-CONVERTING
ZINC (CATALYTIC) (BY SI
BY SIMILARITY
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                                                                        SIMILARITY).
                                                                                      ENZYME
                     (POTENTIAL)
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ACE_HAD IO ACE_H ID ACE_H ID ACE_H ID ACE_H ID ACE_H ID IO 10.00 ID IO 10.00 ID ID IO 10.00 ID ANGIO DE CAIDO GN ACE.

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                                                                                              ACE_HAEIE STANDARD; PRT; 611 AA. 010715; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Angiotensin-converting enzyme precursor (EC 3
         Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Musconorpha; Muscoldea; Muscidae; Haematobia
   NCBI_TaxID=34678;
                                                                                      carboxypeptidase I) (Kininase
                                                           Haematobia irritans
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CONFLICT
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                                                                                                                                                                                                                                                                                          N--KNSFVGWST 608
                                                                                                                                                                                                                                                                                                                 LDNCDIYGSARAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE
                                                                                                                                                                                                                                                                                                                                            LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQ 598
                                                                                                                                                                                                                                                                                                                                                                                                      VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP
                                                                                                                                                                                                                                                                                                                                                                                                                                      K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEY
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                                                                                                                                                                                                                                                                                                                                                                         SGIEPPVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVL 186
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A
                      Arthropoda; Mandibulata; Pancrust
Neoptera; Endopterygota; Diptera;
                                                        exigua (Buffalo fly)
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71025 MW;
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WAYG -> GPMR (IN REF. 3).
C -> S (IN REF. 3).
A -> G (IN REF. 3).
S -> T (IN REF. 3).
V -> M (IN REF. 3).
R -> A (IN REF. 3).
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Pred. No. 6.9e-69;
                                                                                     precursor II).
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                                    Pancrustacea; Hexapoda;
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                        Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 QRIFKEAEKFFVSVGLPNMTQGFWENSMLTDDGNVQKAVCHPTAWDLG-KGDFRILMCTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00791; PEPDIPTASEA ProDom; PD004184; Peptidase_N
                                                                                     237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L43965; AAA70427.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                                      246
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                                                                                                                                                                                                                                                                                              128
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SEQUENCE FROM N.A.
MEDLINE-96215437; PubMed-8647080;
                                                                                                                                                                                                                                                                                                                                               128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wijffels G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C., Kemp D.J., Willadsen P.;
                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                               68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
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                                                                        YRLNKFYGDEVVSKTGPLPMHLLGNMWAQQWSSIADIVSPFPEKPLVDVSDEMVAQGYTP
                                                                                                                     AKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDA
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                                                                                                                                                                                NTKSAKLNNFTDGAEVWLDEYE---
                                                                                                                                                                                                                           KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIED-VEHTFEEIKPLYEHLHAYVR
                                                                                                                                                                                                                                                                              AKVRVCDYKNSAKCDLSLDPEIEEIITKSRDPEELKYYWTQFYDKAGTPTRSNFEKYVEL
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371 371
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196 196
531 531
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246;
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RA KUNDLINE-9804403; PubMed=93847/;
RA KUNSTE F. Ogdsawara N. Moszer I. Albertini A.M. Alloni G.,
RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Galizzi A., Galleron N.,
RA Choi S.K., Codani J.J., Connerton I.F., Ganings N.J., Daniel R.A.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liardinois S., Lauber J., Lazarevic V.,
RA Nonne D., O'Reilly M., Ogdwa K., Ogiwara A., Oudega B., Park S.H.,
RA Nonne D., O'Reilly M., Ogdwa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Rieger M., Rivolta R., Wedler E., Weller E., Valamane K.,
RA Winters P., Wintershi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA Yoshida K., Yoshakashi H., Takemane K.,
RA Wint
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01-OCT-1996
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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical metalloprotease ypwA (EC 3.4.24.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Nature 390:249-256(1997).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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EMBL; Z99115; CAB14125.1;
MEROPS; M32.UPW;
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PROSITE; PS00142; ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L47838; AAB38482.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SubtiList; BG11458; ypwA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 MLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTA----HHEMGHIQYD--MAY 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 YSLTVPF-----GQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENS 331
451 HPIK-----QWLTEKVHIHGKRKKPLDIIKDATG-EELNVRYLIDY 490
                                                                                                                                    394 I---TPQTDAEGILQDVHWAGGDFGYFPSYALGYMYAAQLKQKMLEDLPEFDALLERGEF 450
                                                                540 HKCDISNSTEAGOKLFNMLRL-GKSEPWTLALENVVGAKNMNVRPLLNY 587
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                                                                                                                                                                                                     VVEPVPHDETYCDPASLFHVSNDYS-FIRYYTRTLYQFQFQEALCQ-----AAKHEGPL 539
                                                                                                                                                                                                                                                                         RAINESKPSFIRVEADELTYPLHIIIRYEIEK---AIFSNEVSVEDLPSLWNQKYQDYLG
                                                                                                                                                                                                                                                                                                                                     QEDNETEINFLLKOA--LTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVG 486
                                                                                                                                                                                                                                                                                                                                                                                                          ALSGTNLSDGASMGIHESQSLFYENFIGRNKHFWTPYYKKIQEASPVQFKDISL--DDFV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQPFLLRNGANEGFHEA-----VGE-----IMSLSAATPKHLKSIGLLSPDF- 428
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GLGB_BACSU RESULT 12

GLGB_BACSU P39118;

STANDARD;

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01-FEB-1995 01-FEB-1995 15-JUN-2002

(Rel. 31, Created)
(Rel. 31, Last sequence update) (Rel. 41, Last annotation update)

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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bros. S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Hagga K., Haiech J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sekowska A., Serror S.J., Serror F., Shin B.S., Soldo B.,
RA Rateuchi M., Jenakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Voshikawa H.F., Zumstein E., Yasumoto K., Yata K.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                        Nature 390:249-256(1997).

-1- FUNCTION: CATALYSES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC LINKAGES IN GLYCOGEN BY SCISSION OF A 1,4-ALPHA-LINKED OLIGOSACCHARIDE FROM GROWING ALPHA-1,4-GLUCAN CHAINS AND THE SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98048467; PubMed=9387221;
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"Glycogen in Bacillus subtilis: molecular characterization of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94195107; PubMed=8145641;
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Bacteria; Firmicut
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                                                    PATHWAY: Glycogen biosynthesis; third step.
INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON
SOURCES THAT ALLOW EFFICIENT SPORULATION.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                      CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                              KNOWN AS THE ALPHA-AMYLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Firmicutes;
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01-APR-1993 (Rel. 2
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MEDLINE=92155237; PubMed=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis.
Plasmid pTu 32.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Analysis of genes involved in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X62386; CAA44253.1; -
                                                                                                                                                                                                                                                    405
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SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH, AND ANCHORED TO THE CYTOPLASMIC SIDE OF THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO B. SUBTILIS SPAB AND L. LACTIS NISB.
                                                                                                                                                                                                                                                                                 DKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                                                                                                                                                                                                                                                                              NTNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSE 110
                                                                                                                                                                                                                                                                                                                                                                              ISEAAYILWLLSPNHFGTKTIRNYHEFFMDKYGFEQLVNLKQLLSDINGFGYPKKDSYSF 379
                                                                                                                                                                                                                                                                                                                                                                                                           MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
TEEGIDSLPFCPRIIYKNIILKPATWKINSEMFSE---TENWLNRFATI-REKWHIPKDV
                                                                                                                                                                                                                    EVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF
                                                                                                                                                                                                                                                    EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPN
                                                                                                                                                                                        --GNSIKG-YEDFAVISPILGSFNAGATFGRF-TGNFNIK---
                                                             IDINDIFIGATENKLYLYSEKHDSRIVFVSNSMFNYEFGSELYKFLREISFEKTKFIQPI
                                                                                          IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQG-----
                                                                                                                           -----HYNNYMNENGLEISQLNEGPLNSRNVNILNN--NRIYNTCLNLNLP----KSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          986 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 120;
                                -----VQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25, Created)
25, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                  ----YLLAIQNNSHIEITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116708 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 123;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epiB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              258;
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RESULT 14
BGAL_BACME
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052847;
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                                                                                                                                   EMBL; AJ000733; CAA04267.1; -.
                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                   Strey J.
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DSM 319;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus megaterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 YEILKKEFPNLHEELFNKISILENLKKTLQKSLYTSRSRIIGSFIHMRCN----RIFGIN
                                                                                                                                                                                                                                                                                    mitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. CATALTYIC ACTIVITY: Hydrolysis of terminal, non-reducing galactose residues in beta-D-galactosides. SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEQSFIIPKNRNKHFNNLKDWFSIHLSIPKTYQD-----NFIQDYLLPFITELKVNNFIN
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                                                                                                                   P00722;
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                                                                                                                      1BGL.
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InterPro: IPR004200; Bgal_small_C. InterPro: IPR004199; Bgal_small_N. InterPro: IPR001649; GH_2. InterPro: IPR001649; GH_2. InterPro: IPR001649; GH_2. InterPro: IPR00703; Glyco_hydro_2_C; 1. Pfam; PP002836; Glyco_hydro_2_C; 1. Pfam; PF002837; Glyco_hydro_2_N; 1. Pfam; PF002929; Bgal_small_N; 1. Pfam; PF02930; Bgal_small_C; 1.

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RESULT 15
OSH2_YEAST
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                         OSH2_YEAST STANDARD; PRT; 1283 AA. Q12451; P89891; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Oxysterol-binding protein homolog 2. OSH2 OR YDL019C OR D2845.
                         Urrestarazu L.A., Andre
Submitted (JUL-1996) to
                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
SUBCELLULAR LOCATION
                                                                      SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=4932;
                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                           STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Glycosidase.
ACT_SITE 481 481
ACT_SITE 547 547
SEQUENCE 1034 AA; 118
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PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                                                  717 L 717
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                                                                                                                                                                                                                                                                                                                                                                                    TVE----KNG-----ELVEKHASLLNVAPDGTDELTLSYPLYEQENETD-EFVLTLSLR
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                                                                                                                                                                                                                                                                                                                                                              I 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPKIAEVKKCYQPVKWTAVDPAKGKFAV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILQGGFIWD-----WKDQALQATAEDGTSYLAYGGDFGDTPN-DGNFCGNGLIFADGTA 623
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                     B., Vissers S.;
the EMBL/GenBank/DDBJ databases
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Best Local
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PROSITE; PS50297; ANK REP_REGION;
PROSITE; PS01013; OSBP; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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         247
                                                 644 KRLVDMVSKQGDVNNVW-----VQSVKELEMELSNKTERLASIDKERRGLKKILH----K
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                                                                                                                                                                                       584
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InterPro; IPR001849; PH.
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Beh C.T., Cool L., Phillips J., Rine J.;
"Overlapping functions of the yeast oxysterol-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine T.P., Munro S.;
"Dual targeting of Oshlp, a yeast homologue of oxysterol-binding protein, to both the Goldi and the nucleus-vacuole junction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002110; ANK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 SLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASW---NYNTNITEENVQ---NMN 63
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      KLMNAYPSYISPIGC-----
                                                                                                                                                                       GPYKEKLDMYEQAISIELSSLIELIEQEEPSPEVWLTIKKSLINTSTIFGKLKDLTYKRD 643
                                                                                                                                                                                                                                     LDYNERLWAWESWRS-----EVGKQLRPLYEEYVVLKNEMAR-----
                                                                                                                                                                                                                                                                                             NGANLSQSNTTTGSTASLSDNNYIDNFEGDEANSDDEEEDL----GINFDRDEEYIKAQY 583
                                                                                                                                                                                                                                                                                                                                                     RLNTILNTMSTIYST-----GKVCNPDNPQECLLLEPGLN-----EIMANS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAGDKWSAFLKEQSTLAQMYP------LQEIQNLTVKLQLQALQQNGSSVLSE-DKSK 114
                                                                                                            -----ANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRA
                                                                                                                                                                                                                                                                                                                                                                                                                   ESGKRFVSKMIENRLDGSKTPVGVHTGSALQRVRSSNT-LKSNRSMQSGSGVASPIDKVP
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PF01237; Oxysterol_BP; SM00248; ANK; 2.
; SM00233; PH; 1.
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386
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18.9%; Pred. No. 2.5
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-LPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAM
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         Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourcs J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McLean J., Wooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAMB_SCHPO STANDARD; PRT; 3655 AA. Q10064; Q10064; Q1-FEB-1996 (Rel. 33, Created) Q1-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein CIF5.11c in chromosome I SPACIF5.11c.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
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                                                                                                                                                                                                                                                  MEDLINE=21848401; PubMed=11859360;
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Hypothetical protein; Transferase; Kinase.
DOMAIN 3324 3655 PI3K/PI4K (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02259; FAT; 1.
Pfam; PF02260; FATC; 1.
SMART; SM00146; PI3KC; 1.
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-!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 415:871-880(2002).
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                                             2906 EANQAFATAVQIDIGSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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  398 --EGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYM 455
                                                                                                                                                                                 294 TDAMVDQAWDAQRIFKEAEKFFVSVGLPNMT------QGFWENSMLTDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ENVQNMNNAGDKWSAFLKE--QSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SSWLLLSLVAVTAAQSTIEEQAKT---FLDKFNHEAEDLFY----QSSLASWNYNTNITE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                        KPLYEHLHAYVRAKLMNAYPSYTSPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RINTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWA-WESWRSEVG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDW-----STEQDTLEKATKSLSPFTSLRRHTADALLYLNKTQRKMGSVTEFSRIID 2684
                                                                                                                                                                                                                                                                                                                        KSINKVFLPLVSIAQQSTNKSNTNSVSYLYRGYHEL---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECMQFSLR---RWQQLPKRVYQSHVSLLHHFQEIVEL-----QEAFGIYSQLNDT 2731
                                                                                                                                      QEAFLKLREQAECHYESPSEMQLGLEVINNTNLMYFRNRQKAEFFTLKGMFQN-RLGEKD 2905
                                                                                                                                                                                                                                                                                                                                                                   KQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEI 233
                                                                                      NVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGAN 397
                                                                                                                                                                                                                                 -----AWIINRF-AHVARVHHLPEVCINQL----TKIYTL-----PNIEI 2846
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IPR000403; PI3_PI4_kinase
IPR001440; TPR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 119.5; DB 1; 17.0%; Pred. No. 11;
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                                                -----KAWSEWG-LYHDELFQANPQEIHHACN
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                                                                                                                                                                                                                                                                                        Pfam; PF03028; Dynein_heavy; Motor protein; Microtubules;
                                                                                                                                                                                                                                                                                                                                                          The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kandl K.A., Forney J.D., Asai D.J.;
"The dynein genes of Paramecium tetraurelia: the structure and expression of the ciliary beta and cytoplasmic heavy chains.";
Mol. Blol. Cell 6:1549-1562(1995).
-I- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERMEDIATE AND LIGHT CHAINS.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                       InterPro;
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dynein heavy chain, cytosolic (DYHC). DHC-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2949 AVSCFLQA-SSLLSSSNSKPLLTRVLWLLSVDDSHGSVSEV------VSSFKSE 2995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANELLES ALONG MICROTUBULES.
SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDY-SFIR 514
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                                                                                                                                                                                                                                                                                                                   IPR004273; Dynein_heavy.
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   2.8%;
                                                      MICROTUBULE-BINDING (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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ATP (POTENTIAL).
ATP (POTENTIAL).
Score 119.5;
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DB 1;
Length 4540;
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AC DT DT DT DT DT

15-JUL-1999 (Rel. 38, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable methylenetetrahydrofolate reductase
C06A8.1.

(EC 1.5.1.20).

RESULT 18 MTHR_CAEEL

MTHR_CAEEL Q17693;

STANDARD;

PRT;

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1237 KYEKCSQAKEILKMDP---PTHQQKLNVLL 1263
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                                  714 AFRLNDNSLEFLGIQPTLGPPNQPPVSIWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 YNERLWAWESWRSEVG-----KQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 ----LKTVHKDIQSLQNKFKE--TYQKSQNSRLASARDIPLTSGFVIWSKQLQIRLQKYM 628
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                                                                       NNIQSKI----QQDERYLNQQIQEIEEQWKTSKPDSGDCSPNEAEQILKSLNEQLISVQE 1236
                                                                                                                 LKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPR--TEVEKAIRMSRSRIND 713
                                                                                                                                                        K-KFPGWSADIESFKNGQKVLDRQRYQYPGDWLSFEQVEMQWNQFKQIRSKKLQSQESEM 1180
                                                                                                                                                                                                   KNSFVGWSTDWSPYAD-QSIKVRISLK---SALGDKAYEWNDNEMYLFRSSVAYAMRQYF 655
                                                                                                                                                                                                                                          ····NHFGNKFGEQLRVFN------KNVTTEKEKLLKINFQDLTSDIIESITIIQEQD 1121
                                                                                                                                                                                                                                                                                                                                                                -----TYCDPASLFH---VSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCD 543
                                                                                                                                                                                                                                                                                                                                                                                                           QL-----LE------DMEQYVQTWLNYQSLWELD---IKQVEQILQDDIEKWQQM 1027
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                                                                                                                                                                                                                                                                                    ISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAK----NMNVRPLLNYFEPLFTWLKDQN 599
                                                                                                                                                                                                                                                                                                                             LTDIKQGRATEDNSTTEEHFGAIIIDYRMVQVKINHKYDAWHKELL------ 1073
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + NADP(+) = 5,10-methylenetetrahydrofolate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Flavoprotein; SEQUENCE 663 AA; 75486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02219; MTHFR; 1.
TIGREAMS; TIGRO0677; fadh2_euk; 1.
TIGREAMS; FIGRO0677; fadh2_euk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004621; Fadh2_euk.
InterPro; IPR003171; Mehydrof_redctse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39849; AAA81048.2; -. HSSP; P00394; 185T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 QRIFKEAEKFF------VSVGLPN------MTQG-----FWENSMLTDPGNVQK- 341
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SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: FAD (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSSSIAASMLDYCGVDTMLHMTCVQYNKADTLKHLEQAKAMGLRSILALRGDLPPGTEL 180
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                                                                                                                                                                                                                                                                                                                                                                                          AKLSQLEIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQLFFEAETFEKFVRDCREIGITQP--------IIPGIMPIMGYESIKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIMSLSAATPKHL---KSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFT-YMLEKWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDTHQFRALDMIRWIREEYGNYFSIGCAGYPLGHPQAP-SYKADLMYLKAKCDAGANFVI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FRILMCTKVTMDDFLT-----AHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAV
                                                            AYEWNDNEMYLFRSSVAYA-MRQYFLK----VKN---QMILFGE-----EDVRVANLKPR 678
                                                                                                                         FPWKNRSQHPIRCLESVRPIY-W--SFRPRSYITRTRDWDQFPNG-------
                                                                                                                                                                                         VGAKNMNVRPL--LNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDK 631
                                                                                                                                                                                                                                                      IE-----MCRRL------LDNGTAPSIHLYTMNREGSIREILKSLGLWKLEGDRV
--RWGNS----SSPAFGDVSSYYLSNLTTVRNADDRLAMFGANIESFEDVK-----R
                                                                                                                                                                                                                                                                                                                      YQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEP-----WTLALENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
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18.3%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163; Indels 210;
                                                                                                                                                                                                                                                                                                                                                                                          ----DDAVQKYGTERC
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REPRESENTED TO SERVICE STREET 
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-Kinase anchor protein 9 (Protein Kinase A anchoring protein 9)
16-Kinase anchor protein 450 kDa) (ARAP 450) (A-kinase anchor protein 450 kDa) (ARAP 450) (A-kinase anchor protein 9)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS MEDLINE-99219864; PubMed-10202149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98151389; PubMed=9482789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKA9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 VFINYITQAPN--ADGVKVTVLPWTEAETGVQPETSLISEQLVWCNENGILTVNSQPSVN 505
                                                                                                                                                                                                                                                  "AKAP350, a multiply spliced protein kinase A-anchoring protein associated with centrosomes.";
J. Biol. Chem. 274:3055-3066(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of a cDNA encoding an A-kinase anchoring protein located in the centrosome, AKAP450."; EMBO J. 18:1858-1868(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witczak O., Skaalhegg B.S., Keryer G., Bornens M.,
Jahnsen T., Oerstavik S.;
                                                                                                                                                                                                                                                                                                                                                                             Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G. Trotter K.W., Milgram S.L., Goldenring J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Gastric parietal cell;
MEDLINE=99115654; PubMed=9915845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anchors multiple signaling enzymes to centrosome and the golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 GAPSTDPLVGW 516
    Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                            TISSUE=Lymphoblast;
Hinds K., Sutterer C., Becker M., Hawkins M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kemmner W.A., Deiss S., Schwarz U.;
"Cloning of Hyperion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apparatus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mukai H., O"Characterization of a novel giant scaffolding protein, CG-NAP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99287934; PubMed=10358086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain
                                                                                   Hinds K
                                                                                                                                                                       SEQUENCE OF 1802-3876 FROM N.A. (ISOFORM 5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUG-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274:17267-17274(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
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RA WU X., Graves T., Bradshaw H.;

RA WU X., Graves T., Bradshaw H.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

CC -I- FUNCTION: BINDS TO TYPE II REGULATORY SUBMUTIS OF PROTEIN KINASE CC .

CC -I- FUNCTION: BINDS TO TYPE II REGULATORY SUBMUTIS OF PROTEIN KINASES AND GOLGI APPARATUS WHERE PHYSIOLOGICAL CC PHOSPHATASES ON CENTROSOME AND GOLGI APPARATUS WHERE PHYSIOLOGICAL CC SUBSTRAYES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-CC SUBSTRAYES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-CC JUNCTION (NNJ) AS WELL AS IN NEURONAL SYNAPSES EXPLAINING THAT ITS CC AND THE INTERACTS WITH THE REGULATORY REGION OF PROTEIN KINASE N (PK), PROTEIN PHOSPHATASE 2A (PP2A), PROTEIN PHOSPHATASE 1 (PP1)

CC AND THE INMATURE NON-PHOSPHORYLATED FORM OF PKC EPSILON.

CC -I- SUBCELLULAR LOCATION: CENTROSOMAL IN MANY CELL TYPES AND
                 DOMAIN
DOMAIN
                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                        DOMAIN
                                                                                                         Genew;
                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 17-1800 FROM N.A. Wu X., Graves T., Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prediction of the coding sequences of unidentified human genes, XI. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milgram S.L., Goldenring J.R., Schmidt P.H.;
"AKAP350: A multiply spliced family of proteins with centrosomal
association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                     CAUTION: REF.6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.
CAUTION: REF.9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR
                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN SKELETAL MUSCLE AND IN PANCREAS.

DOMAIN: RII BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC IN PARIETAL CELLS.
ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1
                                                                                                                                                                                                                                                                                                             FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.
                                                                                                                                        AC004013;
AF091711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro
                                                                                                                   AC000066;
                                                                                                                              AB018346;
                                                                                  coll;
                                                                                                                                                                                                                                                                                                                                                                                                                        NATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-4/YOTIAO, 5 AND 6/AKAP350; ARE PRODUCED BY ALTERNATIVE
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                                                                                Alternative
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                                                                                                                                                AAB96867.1; ALT_FRAME.
                                                                                                                              BAA34523
                                                                                                       AKAP9
                                     914
1022
1185
                                                                               splicing;
Plicing; Polymorphism.

PKA-RII SUBUNIT BINDING DOMAIN.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).
                                                                                                                ALT_FRAME
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1154 ALCSLKEELIFAQEEKIKELQKIHQLELQTMKTQETGDEGKPLHLLIGKLQKAVSBECSY 1213
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                                                                   FLQTLCSVLGEYYTPALKCEVNAEDKENSGDYISENEDPELQDYRYEVQDFQENMHTLLN 1273
                                                                                                                                              RLNTILNTMSTIYSTGKYC-----NPDNPQECLL--LEPGLNEIMANSLDYNE-----
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-----RLWAWES--WRSEVGKQLRPLYE-EYVVLKNEMARANHYEDYG
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Pred. No.
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VFGFYNMCFSTLC -> GSSIPELAHSDAYQTREICSS
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MISSING (IN ISOFORM 3)
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QLQEEI -> LATRRD (IN ISOFORM 4).
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RESULT 20
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                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                  Structure 7:1539-1546(1999).
-!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE (BY SIMILARITY TO DYSTROPHIN).
-!- SUBCELLULAR LOCATION: NEURONUSCULAR JUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The 2.0-A structure of the second calponin homology domain from the actin-binding region of the dystrophin homologue utrophin."; mol. Biol. 285:1257-1264(1999).
                                                    EMBL; X69086; CAA48829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 31-256.
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Utrophin (Dystrophin-related protein 1) (DRP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Crystal structure of the actin-binding region of utrophin reveals head-to-tail dimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kendrick-Jones J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keep N.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
MEDLINE=99141377; PubMed=9887274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tinsley J.M., Blake D.J., Roche A., Fairbrother U., Riss J., Byth B.C., Knight A.E., Kendrick-Jones J., Suthers G.K., Love D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=93096045; PubMed=1461283;
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P46939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards Y.H., Davies K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primary structure of dystrophin-related protein.";
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                                                                                                                                                                                                                                          ABP-120, ABP-180, OR BETA-FODRIN).
SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
SIMILARITY: CONTAINS 1 WM DOMAIN.
SIMILARITY: CONTAINS 20 SPECTRIN REPEATS.
SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: MUSCLE.
SIMILARITY: STRONG, TO DYSTROPHIN.
SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
S28381; S28381.
1BHD; 16-FEB-99
1QAG; 01-JAN-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR DMDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTEEYNKLLVLQTRLSKIWGQQTDGMKLEFGEENLPKEETEFLSIHSQMTNLE-----
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PROSITE; PS00019; ACTININ_1; 1.

PROSITE; PS00020; ACTININ_2; 1.

PROSITE; PS50021; CH; 2.

PROSITE; PS50021; WH_DOMAIN_1; 1.

PROSITE; PS501159; WH_DOMAIN_2; 1.

PROSITE; PS501357; ZF_ZZ_1; 1.
                                                                                                                                                                 REPEAT
DOMAIN
ZN_FING
                                                                                       2533 LDDMNQRWNDLKAKSASIRAHLEASAEKWNRLLMSLEELIKWLNMKDEE----LKKQMPI 2588
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                        2640 RNLQSKTELTPEERAQKIAKAMRKQSSEVKEK---WESLNAVTSNWQKQVDKALEKLRDL
                                                       2589 GGDVPALQLQYDHCKALRRELKEKEYSVLNAVDQARV-----FLADQPIEAPEEPR
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183 YVVLKNEMARANHYEDYGDYWR--GDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240 : : | | : | | | | | |
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                                                                                                        29 LDKFNHEAEDL-----FYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                        AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ
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PF00397; WW; 1
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Similarity 18.5%;
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IPR001715; Calponin-like.
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| Sea Job | Qу | dq VQ | Qу Вь | Дb | Db Qq | ОУ ДЪ | Qy Db | ₽ 8 | dq Qy | Db |
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| Search completed: March 13, 2003, 16:57:36 Job time : 43 secs | YEEPLETWLKDQNKNSFYGWSTDWSPYADQS 617 | EGPLHKCDISNSTEAGOKL-FUMLRLGKS-EPWTLALENVVGAKUMUVR-PLLU 586 | EMKREIVGVVEPVPHDETYCDDASLFHVSNDYSPIRYYTRTLYQFQFQEALCQAAKH 535 :::: :::: ::::::::::::::::::::: | | EAVGEINSLS | 357RILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFH 401 | ENSMITDPGNVQKAVCHPTAWDLGKGDF 356 | MVDQAWDAQRIFKEAEKFFVSVGL | HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGREWTULYSLTVPEGQKPUIDVTDA 296NEKVKTVNDLSSQLSPLDLHPSLKMSRQLDDLNMR-W-KLLQVSVDD 2790 | 2697 QGAMDDLDADMKEAESVRNGWKPYGDLLIDSLQDHIEKIMAFREEIAPI 2745 |

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_numan:*
5: sp_numan:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_verteb;
14: sp_urclass
15: sp_urclass
15: sp_urcheap
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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4291
1 MSSSSWLLLSLVAVTAAQST.....ISKGENNPGFQNTDDVQTSF 805
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            sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Match Length DB | BB | ij | Description |
|---------------|--------|----------------|-----------------------|----|--------|--------------------|
| 1 | 4291 | 100.0 | 805 | 4 | Q9NRA7 | O9nra7 homo |
| N | 4288 | 99.9 | 805 | 4 | Q9BYF1 | 09byf1 homo |
| w | 4281 | 99.8 | 804 | 4 | 09UFZ6 | |
| 4 | 3579 | 83.4 | 805 | 11 | Q8R010 | 0 |
| ر ت | 3485 | 81.2 | 798 | 11 | Q99N71 | Q99n71 mus |
| σ | 1539 | 35.9 | 353 | 11 | Q99N70 | 099n70 mus |
| 7 | 1336 | 31.1 | 732 | σ | Q9GLN6 | Q9qln6 pan |
| œ | 1329 | 31.0 | 1304 | 0 | Q9GLN7 | 09qln7 pan |
| 9 | 1310 | 30.5 | 1313 | 11 | Q9EQM9 | Q9eqm9 rattus norv |
| 10 | 1303 | 30.4 | 694 | 4 | Q15540 | Q15540 home |
| 11 | 1089.5 | 25.4 | 648 | ហ | Q9NDS8 | Q9nds8 bombyx mori |
| 12 | 1086 | 25.3 | 615 | υ | Q9NKE4 | Q9nke4 drosophila |
| 13 | 1057 | 24.6 | 660 | G | Q17248 | |
| 14 | 1030 | 24.0 | 630 | u | Q24222 | Q24222 drosophila |
| 15 | 1028 | 24.0 | 630 | 5 | Q9VLJ6 | 09vlj6 drosophila |
| 16 | 1004 | 23.4 | 249 | _ | 20000 | |

| 41 42 43 45 | 38 | ωωω 4 70 70 10 10 10 10 10 10 10 10 10 10 10 10 10 | 332 332 | 28 29 30 | 25 4 4 | 17 18 19 20 21 21 |
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| 127.5 127.5 127 127 125.5 124.5 | 139.3 139 136 130.5 | 152.5 147 147 | 239 157 154 | 306.5 280.5 251.5 | 409.5 408.5 390 387 | 930 841 642.5 502.5 476 434.5 |
| 22.00 | | | 3.7 3.6 | 5.5 | 0999 | 21.7 19.6 15.0 11.7 11.7 |
| 3571 3574 779 600 987 | 987 608 611 461 | 734 54 502 | 532 502 | 121 135 157 | 222 222 222 222 | 844 792 907 661 611 |
| 10 16 11 | 16 2 | 1000 | 16 16 | 11461 | 14155 | 125555 |
| Q9SL27 Q9AUB4 Q9XYS8 Q8R670 Q61636 | Q9PR80 Q9PPW8 Q9PPW8 Q9KI52 | Q9NKE3 Q95161 Q92AC3 | Q9TX66 Q9KFV0 08Y616 | Q9BDG1 Q9BDG1 Q16425 Q61265 | Q9ESG3 Q9ESG3 Q9ESG3 | Q8SXX2 Q9VJV1 Q18581 Q18581 Q9V520 Q9VJV2 Q9VJV2 |
| Q9s127 arabidopsis Q9aub4 arabidopsis Q9ays8 dictyosteli Q8r670 fusobacteri Q61636 mus musculu | урумдо анадаена sp Q9pr80 ureaplasma Q9ppW ureaplasma Q9k152 enterococcu | Q9nke3 drosophila Q95161 canis famil Q92ac3 listeria in | Q9tx66 drosophila Q9kfvO bacillus ha Q8y616 listeria mo | QJ6425 mus musculu Q9bdq1 bos taurus Q16425 homo sapien Q61265 mus musculu | Q9WUZI drosophila Q95u59 drosophila Q9esg3 rattus norv Q9hbj8 homo sapien | |

ALIGNMENTS

| DR KW | DR DR | DR | | DR | DR | RI. | RT | RA | RA | RA | 장 | RN | ۲. | RΤ | RT | RA | RA | RC | RP | RN | ox X | 8 | റ്റ | SO | DE | DE | DT | Τď | DΤ | AC | IJ | RE Q9: |
|--|---|------------------------------------|--|-------------|------|--|--|------|--|----|----------------------|----|--|------------|---|-------|--|----|--------------------|-----|------------------|----------------------------------|---|-----------------------|-------------|---|----------------------|---|--------------------------------------|----|----------------------------------|-----------------|
| ProDom; PD004184; Peptidase_M2; 1. PROSTTE; PS00142; ZINC_PROTEASE; UNKNOWN_1. Carboxypeptidase. | Pfam; PF01401; Peptidase_M2; 1. PRINTS; PR00791; PEPDIPTASEA. | InterPro; IPR000130; Zn_MTpeptdse. | MERCPS; MOZ.006; InterPro: IPR001548: Pentidase M2 | AAF99721.1; | AF24 | angiotensini~9."; Circ. Res. 0:0-0(2000). | "A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to | S. ; | o N., Donovan M., Woolf B., Robison K., Jeyaseel | | SECTION OF FROM N. A | | Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. | Carboxypep | "A Human Homolog of Angiotensin Converting Enzyme - Cloning and | A.J.; | Tipnis S.R., Hooper N.M., Hyde R.J., Christie G., Karran E., | | SEQUENCE FROM N.A. | [1] | NCBI_TaxID=9606; | Primates; Catarrhini; Hominidae; | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | HOMO sapiens (Human). | idase ACE2) | Angiotensin converting enzyme-like protein (ACE-related | (TrEMBLrel. 19, Last | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | 01-OCT-2000 (TrEMBLrel. 15, Created) | • | Q9NRA7 PRELIMINARY; PRT; 805 AA. | RESULT 1 Q9NRA7 |

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01-JUN-2001
01-JUN-2002
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  sapiens (Human)
                                                                                             YASIDISKGENNPGFQNTDDVQTSF
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Similarity 100.0%;
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Submitted (APR-2001) to the
EMBL; AB046569; BAB40370.1;
MEROPS; M02.006; -
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QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                       NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
PROSITE; PS00142; PS00142; DZAAB4C2708
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the EMBL/GenBank/DDBJ
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Pred. No. 5.8e-305;
1; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 92.3 kDa protein (Fragment).
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EMBL; AL110224; CAB53682.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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InterPro; IPR000130; Zn_MTpeptdse.
pfam; pF01401; Peptidase_M2; 1.
pRINTS; PR00791; PEPDIPTASEA.
proDom; PD004184; Peptidase_M2; 1.
pROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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                          TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEINSLSAATPKHLKSI 421
                                                                       WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
                                                     WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RIKEN cDNA 2010305L05 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482
                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026801; AAH26801.1; .
SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8R0I0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08R0I0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 LEELGIQPTLGPPNQPPVSIWLIVEGVVMGVIVVGIVILIETGIRDRKKKNKARSGENPY 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 ASIDISKGENNPGFQNTDDVQTSF 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 ASIDISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                          241
                                                                                                                                121 NTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEYGKQLRPLY 180
 241
                                                       181
                                                                               181
                                                                                                                                                             61
                                                                                                                                                                                      61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                               1 MSSSSWILLISLVAVTTAGSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQ 60
                                                                                                                                                                                                                                         1 MSSSSWLLLSLVAVTAAOSTIEEQAKTELDKFNHEAEDLFKOSSLASWNYNTNITEENVO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFYGWSTDWSFYADQSIKYRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKYKNQ 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFYGWSTDWSDYADQSIKYRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKYKNQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDISNSTEAGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLETWLKDQNKN 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEFIGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPY 780
                                                                                                                                                            KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
                                                                                                         HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ 300
                                                  EEYVVLKNEMARANNYNDYGDYWRGDYEAEGADGYNYNRNOLIEDVERTEAEIKPLYEHL
                                                                              EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                                                                                       661;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                   83.4%; Score 3579; DB 11; Length 805; 82.1%; Pred. No. 4.2e-253;
                                                                                                                                                                                                                                                                          60; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 AA.
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            Best Local Similarity
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                                                                                                         Carboxypeptidase.
SEQUENCE 798 AP
                                                                                                                                        PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase M2; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                     Pfam; PF01401; Peptidase_M2;
                                                                                                                                                                                                                                                                                           InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB053181; BAB40431.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y., Hida M., Tanigami A., Muroi S.; "Molecular cloning, mRNA expression, and chromosomal localization of mouse Anglotensin converting Enzyme-Related Carboxypeptidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; M
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001680; WD40
                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1917258; 2010305L05R1k.
InterPro; IPR001548; Peptidase_M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99N71;
Q99N71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2010305L05RIK OR ACE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 YASIDISKGENNPGFQNTDDVQTSF 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
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                                                                                                   798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                             91943 MW;
            81.2%;
82.2%;
Pred. No. 3.1e-246;
                           Score 3485; DB 11;
                                                                                403AEA29D55725A4 CRC64;
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                        Length 798;
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
         NCBI_TaxID=10090;
                                                           Mus musculus (Mouse)
                                                                                 Anigotensin-converting enzyme-related carboxypeptidase.
                                                                                                                                                                                     Q99N70
                                                                                                                                                                   Q99N70;
                                                                                                                                                                                                                                                                                                                        721 SLEFLGIHPTLEPPYQPPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREESP
                                                                                                                                                                                                                                                                                                      781 YAS 783
                                                                                                                                                                                                                                                                       781 YDS 783
                                                                                                                                                                                                                                                                                                                                                                                                             661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 CTKVTMDNFLTAHHEMGHIQYDMAYARQPFLLRNGANEGFHEAVGEINSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GWDAERIFQEAEKFFVSVGLPHMTQGFWANSMLTEPADGRKVVCHPTAWDLGHGDERIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AWDAORIFKEAEKFFYSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 HAYVRRKLMDTYPSYISPTGCLPAHLLGDMWGRFWTNLYPLTVPFAQKPNIDVTDAMMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
                                                                                                                                                                                                                                                                                                                                          SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP 780
                                                                                                                                                                                                                                                                                                                                                                                         QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                                                                                                                                                                                                                                                                                                                        QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSFVGWNTEWSPYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCDISNSTEAGQKLLKMLSLGNSEPWTKALENVVGARNMDVKPLLNYFQPLFDWLKEQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSFYGWSTDWSPYADOSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVKN 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCDISNSTEAGQKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KREIVGVVEPLPHDETYCDPASLFHVSNDYSFIRYYTRTIYQFQFQEALCQAAKYNGSLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMSEAAAKWSAFYEEQSKTAQSFSLQETQTPIIKRQLQALQQSGSSALSADKNKQLNTIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y., Hida M., Tanigami A., Muroi S.; "Molecular cloning, mRNA expression, and chromosomal localization mouse Angiotensin-converting Enzyme-Related Carboxypeptidase."; submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
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InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                     OGGLN6:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Dipeptidyl carboxy peptidase 1 testicular form.
the renin angiotensin system.", Genomics 69:14-26(2000).
EMBL; AF193486; AAG31359.1; -.
EMBL; AF193473; AAG31359.1; JO:
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cianiata, vertebrata, Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                          Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                               Dufour C., Casane D.,
                                                                                                                                                           NCBI_TaxID=9598;
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                                                            "Human-Chimpanzee DNA sequence variation in
                                                                              Jeunemaitre X.;
                                                                                                           MEDLINE=20469400;
                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 AA; 40442 MW; D17B71141EE4AF5B CRC64;
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                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                              PubMed=11013071;
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                                                                                                 Denton D., Wickings J., Corvol P.,
     JOINED
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PRINTS; PR00791; PEPDIPTASEA.

PROSTIE; PS004184; Peptidase_M2; 1.

PROSTIE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 732 AA; 83428 MW; C43D06443A47E74B CRC64;
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InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                  302 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILM 360
                                                                                                                                                                                           461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
                                                                                           541 KCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TSAQSPNLVTDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA 120
640 LHGEKLGWPQYNWTPNSARS 659
                            601 --NSFVGW-STDWSPYADQS 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
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AF193480;
AF193481;
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AF193475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                      KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                          LNILSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                                                                    CTKYTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                     WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ 400
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                                                                                                                           RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
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                                                            KCDIYQSKEAGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENE
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AAG31359.1;
AAG31359.1;
AAG31359.1;
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA,
PRODOM; PD004184; Peptidase_M2; 2.
PRODOM; PD004184; Peptidase_M2; 2.
PROSITE; PS00142; ZINC_PROTEASE; UNK
252 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKFNIDVTDAMVDQAWDAQRIFKE 310
                                                                                           132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 191
                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                   696 --LKYGTQARRFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 753
                                                                                                                                                                 642 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                          72 FIKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                               20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE------NVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the renin angiotensin system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human-Chimpanzee DNA sequence variation in the four major genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20469400; PubMed=11013071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dipeptidyl carboxy peptidase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jeunemaitre X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9598;
                                                                                                                                                                                                                                     loca1
                       RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH 861
                                              RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                      VCHTNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA
                                                                                                                                                                                                                      254;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AF193478;
AF193479;
AF193480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF193486; AAG31358.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF193469;
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                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                   1304 AA;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                          AAG31358.1;
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AAG31358.
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                                                                                                                                                                                                                                31.0%; Score 1329; DB 6; Length 1304; 41.6%; Pred. No. 3.3e-88;
                                                                                                                                                                                                                                                                   149369 MW;
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                DCF728D0BA0F1314 CRC64;
                                                                                                                                                                                                                                                                             UNKNOWN_1.
                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                               3.3e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001348; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase_M2; 2.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1313 AA; 150941 MW; E888341562542B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jafarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A., Corvol P., Sternberg E.M.; "Characterization of a missense mutation in the angiotensin I-converting enzyme cDNA in exudative inflammation resistant F344/N
           140 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF201331; AAG35596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=F344/N; TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                               710 AKTFDVSNFQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG-- 767
                                                                                                                                                                                                                        650 TDEAKANREVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLQKNKEVSNHTLKYGTW 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensin-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9EQM9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1042 SD-EHDINFLMKNALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1100
                                                                                                                                                                                                                                                                     20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITTEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 STDWSPYADQS 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             922 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369
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                                                                                                                                                       AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                         h 30.5%; Score 1310; DB 11; Similarity 42.0%; Pred. No. 8.1e-87;
                                                                                                                                                                                                                                                                                                                                                                           Conservative 115; Mismatches 214; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1313;
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1177 MKLGYSKOWPEAMKIITGOPNMSASAIMNYFKPLTEWLVTENRRHGETLGWPEYTWTP 1234
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                                                                                                                                                                                                                                                                                                                                        angiotensin-converting enzyme.";
proc. Natl. Acad. Sci. U.S.A. 86:7741-7745(1989).
EMBL; M26658; AAA60612.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90046671; PubMed=2554286; Ehlers M.R., Fox E.A., Strydom D.J., Riordan J.F.; "Molecular cloning of human testicular angiotensin converting enzyme: the testis isozyme is identical to the C-terminal half of endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                PTAM; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
SEQUENCE 694 AA; 79333 MW; 57COFF9C5AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
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                                                                                                                                                                                                                                                                                                      InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
109 IKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNG--SCLQLEPDLTNVMATSR 166
                                    97
                                                                      57
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                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDSWRSSYESDDLE-----QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCLSLEPDLTNIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDA 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPSIDATEAMIKQGWTPRRIFKEADNFFTSL 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDPGSKFHVPANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIQYFMQYKDLPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSE-GSGYEHDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLPNMTQGFWENSMLTDPGNVQKAVCHPTAMDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                              LQALQQNGSSYLSEDKSKRLNTILNTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSL 156
                                                                                                      LASWNYNTNITEE-----NVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQ 96
                                                                      IATKNYNTNITTETSKILLQKNMQIANHT-----LKYGTQARKFDVNQLQNTTIKRI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                              Conservative
                                                                                                                                                               30.4%; Score 1303; DB 4; Length 694; 42.7%; Pred. No. 1e-86;
                                                                                                                                                107; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                    57C0FF9C5AECAll9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                694
                                                                                                                                                  195;
                                                                                                                                                  Indels
                                                                                                                                                    34;
                                                                                                                                                    Gaps
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   Дb
                                                            Qy
                                                                                                                                  Matches 232;
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                           InterPro; IPR001548; Peptidase_M2.
InterPro; IPR001319; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase_M2; 1.
ProDom; PD004184; Peptidase_M2; UNF
PROSITE; PS00142; ZINC_PROTEASE; UNF
SEQUENCE 648 AA; 74917 MW; 9A740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NDS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecdysteroid-inducible angiotensin-converting enzyme-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NDS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB026110; BAA97657.1; MEROPS; M02.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         converting enzyme-related gene in wing discs of Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and expression of the ecdysteroid-inducible angiotensin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quan G.X., Mita K., Ok
Kanke E., Kawasaki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C108; TISSUE-WING IMAGINAL DISK; MEDLINE=20556050; PubMed=11102839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 GAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSPYADQS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     576 GQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWPQYNWTPNSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insect Biochem. Mol.
                                                            11 LVAVTAAQSTIEEQAK-TFLDKENHEAEDLFY------QSSLASWNYNTNITEEN 58
                                                                                                                                                                Local
10 LIAAIVAVFIVATQGRDPDLEAREHEAREYMLHLDKATGLRKNRASLAEWEYTSNITKEN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYETPSLE--- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFW 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKEADDFFTSLGLLPVPPPEFWNKSMLEK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFYSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLATAMKLGFSRPWPEAMQLIT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIR 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALRE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRN 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYTRTLYOFOFOEALCOAAKHEGPLHKCDISNSTEAGOKLFUMLRLGKSEPWILALENVV 574
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDLERLFQELQPLYLNLHAYVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTW 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okano K., Shimada T., Ugajin N., Xia Z., Goto N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. 31:97-103(2001).
                                                                                                                                                                    25.4%; score 1089.5; 35.6%; pred. No. 3.96
                                                                                                                                                                                                                                                                     9A740AA9FCACEBF0 CRC64;
                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                No. 3.9e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648
                                                                                                                                                259;
                                                                                                                                                                                                     DB 5; Length 648;
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621
                                                                                                                                                35;
                                                                                                                                                Gaps
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AC CONTRACTOR RANGE RANG
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
                                                                                                                                                                                             Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of prosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                              STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                       Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANCE OR CG8827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NKE4; Q9VJV3;
01-OCT-2000 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NKE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 PLHDWLRAENQRTGEHIGWEPTNMEYCTPSQLSELNVKEPSSSPATQQSDS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 PLFTWLKDQNKNS--FYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 HAAGDPNKKLVDCDIYQSVAAGNALANMLKMGSSKPWPDAMEALTGQREMKADGLLEYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 HYWKLREQLQGVEPPVNRTEDDFDAAAKYHVSSNVEYARYYVSFIIQFQFHRGVCQLAGE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 KWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQ-AAK 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 KNFTDYVNLYNEAAKLNGFDNVAEWWQSEYEVPDFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 TVSGMESNYATAKICSYKNESKCDLSLEPEITEIFSTSQDPEELKHAWVEWHNAAGATAK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEG-----PLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFE 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (LD11258p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHLRRVGLATGD-AEDEQTEINQLYKMGIDKIAFLPFAYTLDLFRYGVFRRKTLPEDYNC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRILMCTKVTMDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRDQNYTPMKMFQMSDEFFRSLNLTAMPEKFWKNSIIEKPTD-REIVCHASAWDFFDGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-D 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRIKQCTTVDYEYFQTTHHEMGHIQYYLQYRDQPVVFRDGANQGFHEAVGDTIALSVSSP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQLHAYVRKRLRDKYGDKVVSARGPIPAHLLGNMWAQTWNNIESFTRPYPDKKEIDVTQA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHLHAYVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILNTMSTIYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKSIQTHLELSRQEKAAWEETKMYGWQDFQDFTLRRMFKKYSQLGVAALPDDKFQALMR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              615 AA
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RAARA 
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                                                              Query Match
                                                                                                                                                     PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouamenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003408; AAF44834.1; -.

EMBL; AE003641; AAF53353.2; -.

EMBL; AY061129; AAL28677.1; -.

FlyBase; FBgn0012037; Ance.
                                                                                                                                                                                                                                                                             Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    615 AA;
                                                                                                                                    70913
            25.3%; Score 1086; 36.4%; Pred. No. 6.
                                                                                                                                MW;
Pred. No. 6.4e-71;
                                                                                                                    9E3691BCC51D6C48 CRC64;
                                         DB 5;
                                 Length 615;
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Matches 223;

Conservative

122;

Mismatches

Indels

22;

9

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RESULT 13
Q1724
ID Q1724
AC Q1724
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-WO
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q17248
Q17248;
                                                                                                                                                                  Whitfeld P.L., Johnson M.C., Smith D.R.J., Sne Brown G.S., Cairns D., Foy A.B., Irving D.O.; "The Cloning of an Angiotensin-Converting Enzy Tick Boophilus microplus."; submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U62809, AAB0498.1;
ProDom; PD004184;
Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLIFE: 01, Created)
01-NOV-1996 (TREMBLIFE: 01, Last sequence update)
01-UNV-2002 (TREMBLIFE: 21, Last annotation update)
Angiotensin-converting enzyme-like protein precursor
                                                                                          Pfam; PF01401; Peptidase_M2; 1. PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6941;
                                                                                                                                                InterPro; IPR001548; Peptidase_M2
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
METALLOPEPTIDASE (Angiotensin-converting enzyme-r
  Taylor C.A.M., Coates D., Shirras A "The Acer gene of prosophila codes enzyme bomologue."; Gene 181:191-197(1996).
                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                               ACER OR CG10593.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNSFVGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HECDIYGEKNAGDVLKKGLSLGRSKPWPDVLEIMAGTRQMSASSLKKYYEPLEKWLDERI 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HKCDISNSTEAGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLKP---TDKYNAVDLLLMSALDKIAFLPFGYLLDKWRWTIFTGETPFDKMNEKFWEYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKMFHAAEDFFTSLGLDNMTSEFWSKSILTKPED-REIQCHASAWNMYNGDDFRIKMCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.6%;
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                                                                                   Shirras A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1057; DB J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =
                                                           for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630
                                                                                                                                                                                                                                                                                                                                       enzyme-related
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                                                           angiotensin-converting
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                                                                                                                                                                                                                                                                                                                                                                  update)
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Best Local :
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                                                                                                                                                  483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01401; Peptidase_M2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0016122; Acer.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                              305
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
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QE--NSRLGVPLGWGP 616
                                  DQNKNSFVGWSTDWSP 612
                                                               LTLDNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEEFTGETEMDPAALLEYFEPLYQWLK
                                                                                                  --LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                                                                                                     AQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT
                                                                                                                                        efggveppvfrtekdfdppakyhidadveylryfaahifqfqfhkvlcrkagqyapnnsr
                                                                                                                                                                                                                  LIE-NGRLDEKSRINQLFKQALSKIVFLPFGYAVDKYRYAVFRNELDESQWNCGFWQMRS
                                                                                                                                                                                                                                                                                         EVDSHYFYVVHHELGHIQYYLQYEQQPAVYRGAPNPGFHEAVGDVIALSVMSAKHLKAIG
                                                                                                                                                                                                                                                                                                                                                                  VQKLFELGDQFFQSLGMRALPPSFWNLSVLTRPDD-RQVVCHASAWDFYQDSDVRIKMCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYATATYCSYTNRSDCSLTLEPHIQERLSHSRDPAELAWYWREWHDKSGTPMRQNFAEYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YARNAELNKRLAQQIKSSDYVQSEDADIRRQAEHLSKLGASALNADDYLALQNAISSMQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLPHGLSMGNSCSASVLE-ARRFFELENEQLRRRFHEEFLSGYNYNTNVTEANRQAMIEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNA
                                                                                                                                                                               EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGP----
                                                                                                                                                                                                                                                      LLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKR 482
                                                                                                                                                                                                                                                                                                                              KVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                          RFRLRQHYGPDVMPAEGNIPISLLGNMWGQSWNELLDLFTPYPEKPFVDVKAEMEKQGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLTRKASQLNGHRSYADYWVQFYE-----DPDFER-----QLDATFKQLLPLYRQLHGYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD004184; Peptidase_M2; 1.

pS00142; ZINC_PROTEASE; UNKNOWN_1.

236 236 L -> F (IN REF. 2).

27 341 341 Q -> H (IN REF. 2).

27 528 528 V -> A (IN REF. 2).

28 630 AA; 73042 MW; 248A4B90319BC32D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%; Score 1030; DB 5; 35.6%; Pred. No. 8.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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havez C., Chew M.,
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RESULT 15

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QPULJA

QPULJA

AC QPULJ

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DT 01-MA

DT 01-MA

DT 01-MA

DT 01-ME

ACER

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                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan R., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003621; AAF52693.1; -.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                          FlyBase; FBgn0016122; Acer
                                                                                                                                               MEROPS; M02.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TIEMBLIEL 13,
01-MAY-2000 (TIEMBLIEL 13,
01-DEC-2001 (TIEMBLIEL 19,
ACER protein (LD28328P).
ACER OR CG10593.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
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RESULT 16
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Q9D836;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; |
ProDom; |
PROSITE;
                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                              2010305L05Rik protein
                  Kawai J.,
                                                                                          NCBI_TaxID=10090;
                                                                                                                                                    2010305L05RIK
                                                                                                                                                                                                                                                                                                                  603
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                                                                                                                                                                                                                                                                                                                  QE--NSRLGVPLGWGP
                                                                                                                                                                                                                                                                                                                                                                      LTLDNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEEFTGETEMDPAALLEYFEPLYQWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTE-NGRLDEKSRINQLFKQALSKIVFLPFGYAVDKYRYAVFRNELDESQWNCGFWQMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQKLFELGDQFFQSLGMRALPPSFWNLSVLTRPDD-RHVVCHASAWDFYQDSDVRIKMCT
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                                                                                                                                                                                                                                                                                                                                                                                                  --LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK
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219; Conserv
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PD004184; Peptidase_M; PS00142; ZINC_PROTEA
                  Shinagawa A.,
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35.6%;
   Fukunishi Y., Konno H.,
                                                                                                                                                                                                                                                                                                                  616
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21,
               Shibata K., Yoshino M.,
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Last sequence update)
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Pred. No. 1.2e-
12; Mismatches
                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                        Muridae;
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 M., Itoh M.
Adachi J.,
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                                                                                                      Murinae;
   Fukuda
                Ishii
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Best Local :
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Q8SXX2;
Q1-JUN-2002
Q1-JUN-2002
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        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Frise George M., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.
                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aizawa K., Izawa M., Nishi K., Kiyosawa Saito T., Okazaki Y., Gojobori T., Bono
                                                                               Stapleton M., Brokstein P.,
                                                                                             STRAIN-BERKELEY;
                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                 Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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InterPro; IPR001548; Peptidase_M2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREENSYDSMDIGKGESNAGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt PRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDNSLEFLGIHPTLEPPYQ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRISTNEEVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEELGIQPTLGPPNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIKVRISLKSALGANAYEWINNEMFLFRSSVAYAMRKYFSIIKNQTVPFLEEDVRVSDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187;
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(TrEMBLrel.)
(TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          249
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Bono H., Kasukawa T.,
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MEDLINE=20196006; PubMed=10/31132, Adams C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                   STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Diptera Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Trac
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
R EMBL; AE003641; AAF53356.1; -.
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Bockova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Books B., Bellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Books A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Barris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Books B., Bellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Books B., Bellian T.J., Hernandez J.R., Houck J.,
Books B., Bellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Books B., Bellian T.J., Hernandez J.R., Houck J.,
Books B., Bellian T.J., Hernandez J.R.,
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 792 AA; 92321 MW; 757EC472089022B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNYNNNPNYEFY-GINNRNRFENPFLSNQDRFNLNQGYLERQRYQQDRRYQQELEKLRIL
PSAWDFCNRHDFRVKICTDINQRSLISVHHEMAHIQYFLQYRHLPKIFRNGANPAFHQAV
                                                PTAWDL-GKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAV
                                                                                                     PGRKLIDVTPRMVEQGYTPQLMFQLAEEFFTSINMSAVGPEFYRNSIFEQPLD-RRVLCE
                                                                                                                                    GQKPNIDYTDAMYDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCH
                                                                                                                                                                                                                DIVWEQIRPLYEGLHAYVRRKLRDYYGPDRINRIAPIPSHILGNMYGQSWSNVLDILIPY
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                                                                                                                                                                                                                                                                                                                         EYHRKAGRGMRDSYEQLIDVMQEVAYVNNVTNGGEYWYLAYE
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30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 841; DB 5; Pred. No. 7.8e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PLQEIQNLTVK 94
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1 H.O.,
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Pfam; PF01401; Peptidase_M2; 1.
ProDom; PD004184; Peptidase_M2; 1.
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01-NOV-1996 (TREMBLrel. 01, Cre.
01-NOV-1996 (TREMBLrel. 01, Las.
01-JUN-2002 (TREMBLrel. 21, Las.
Hypothetical 101.1 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
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ALNRDSKDSTICDKDVPPPCALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYN
                                                                                                                                                                                                                                                                       SSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN
                                                                                                                                                             MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN
                                                                                                                                                                                                                 SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA
                                                   TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE
                                                                                                       LDEAENVLTMFVRSTSMQAKQFDMASVTDEKVMRQLGYVSFEGMSALAPSRFADYSQAQA
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907 AA; 1
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27.0%;
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EMBL/GenBank/DDBJ databases
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R., Cander S., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R., Cander S., Davies P.,
RA Gebart W.D., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbon K.J., Evangelista C.C., Ferraz C., Ferrizer S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
Durbon K.J., Evangelista C.C., Ferraz C., Ferrizer S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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ANCE-4 OR CG8196.
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pullard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
E. Science 287:2185-2195(2000).
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PRODOM; PD004184; Peptidase_M2; 1.
SEQUIENCE 661 AA; 76218 MW; 208
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InterPro; IPR001548; Peptidase_M2.
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134; Mismatches 303; Indels 103;
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Search completed: March 13, 2003, 16:58:02 Job time: 46 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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Gapop 10.0 , Gapext 0.5
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US-08-468-33-2
US-08-468-33-2
US-08-471-18-18
US-09-521-220-18
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Sequence 2, Appli
Sequence 4, Appli
Sequence 7, Appli
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Sequence 11, Appli
Sequence 15, Appli
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Sequence 17, Appli
Sequence 18, Appli
Sequence 18, Appli
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| RESULT 1 US-08-989-299. Sequence 2, Patent No. (GENERAL INI) APPLICANI APPLICANI APPLICANI APPLICANI APPLICANI CORRESPO CORRESPO ADDRESS STREET CITY: STATE: COMPUTER ZIP: COMPUTER CO | | 28 29 31 32 32 33 34 44 44 44 44 44 44 44 46 46 47 48 48 48 48 48 48 48 48 48 48 48 48 48 |
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| 299-2 2, Appl 2, Appl 0. 61945 CANT: RACANT: ROF INVE 00F INVE 00F SEQ SPONDENC RESSEE: BEST: ON Y: BOST NTE: MA NTRY: U 02109 : 02109 IUM TYPE BUTER: | | 101.5 2.4 101.5 2.4 99.5 2.3 99.5 2.3 99.5 2.3 97.5 2.3 |
| Su S | | 550 550 550 550 550 550 550 550 550 550 |
| 89299 E. CONVERTING ENZYME ERAPEUTIC AND DIAGNOSTIC ELIOT LLP Square Square | ALIGNMENTS | US-09-306-593-13 US-09-134-001C-3153 US-09-02-285-84 US-08-953-040-2 US-07-903-466-3 PCT-US93-05-94-3 US-08-747-221B-55 US-09-005-051-55 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-09-005-051-31 US-08-315-844A-22 US-08-315-803-2 US-08-417-803-2 US-08-317-78-80-2 US-08-317-78-80-2 US-08-317-78-80-2 US-08-317-701-27 US-08-317-701-27 |
| HOMOLOG USES THEREFOR | | Sequence 13, Appl Sequence 3153, Appl Sequence 84, Appl Sequence 2, Appli Sequence 3, Appli Sequence 35, Appli Sequence 55, Appli Sequence 31, Appli Sequence 31, Appli Sequence 22, Appli Sequence 2, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli |

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                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-989-299-2
                                                                                                                      Matches 805; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: LEM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-DEC
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/989,299 FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                      MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
                                                                                                                                    100.0%; Score 4291; DB 4; 100.0%; Pred. No. 0;
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US-08-481-626-2
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Patent No. 5801040
                                                                                                                                          APPLICANT: Hubert, Christine
APPLICANT: CORVOL, Pierre
TITLE OF INVENTION: Nucleic Ac
TITLE OF INVENTION: Testicular
TITLE OF INVENTION: Enzyme in
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                  STREET: 1300 I S
CITY: Washington
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                                    STATE:
                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J. 16 REGISTRATION NUMBER: 25,146 REFERENCE/DOCKET NUMBER: 045 TELECOMMUNICATION INFORMATION: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0,
         541
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PRIOR APPLICATION DATA:
                                            520
                                                                                                          461 LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL
                                                                                                                                                        421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-JUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 MSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FR 89-09062 FILING DATE: 05-JUL-1989
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KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 60C
                                  RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
                                                                 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQEQEALCQAAKHEGPLH
                                                                                                                                            IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                 CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS
                                                                                                                                                                                                                    CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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                                                                                                                                                                                                                                                                                                                                 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METTYSVATVCHPNG---SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259;
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41.8%; Pred. No. 4
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TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keitl
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580 KCDIYQSKEAGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENE 639
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                                                                                                                           183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                    173 METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
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LECOMMUNICATION TO
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281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG 340
                                          243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                   231 YVELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHA 280
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                                                                                                                                                                                                                                                                                                                                                                                   15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
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                                                                                                                                                                                                                                                                                             63 NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
                                                                                                                                                                                                                                                                                                                                        61 TSAQSPNLVTDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                            MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
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One Post Office Square
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                                           Matches
                                                               Best
                                                                                    Query Match
                                                                                                                                                                                                                                                                                 TELEFAX: 617-832-7000 TELEFAX: 617-832-7000 7:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
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                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1306 amino acids
                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109-2170
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                                                                                                                                                                                                                                                                                                                                                                                          NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                          STRANDEDNESS:
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20 TIBEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH 579
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                                             255;
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                                             Conservative 118; Mismatches 204;
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                                                                  31.2%; Score 1337; DB 4;
41.7%; Pred. No. 5.9e-119;
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                  ATTORNEY/AGENT INFORMATION: NAME: Arnold E., Beth
                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,299 FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keith E.
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                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
    REGISTRATION NUMBER:
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                                                             CLASSIFICATION:
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                                                                                  GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
APPLICANT: ROBINSON, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                            Sequence 8, Application US/08989299 Patent No. 6194556
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                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
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                                                                                                                                                                                                                                                                                                                                                             596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653
                                                                                                                                                                                                                                                                                                                                                                                           558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK---NSFVGW-STDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                               536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 FIMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 FLLKQALTIVGTLÞFTYMLEKWRMMVFKGEIPKDQWMKKWWEMKREIVGVVEÞVÞHDETY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475
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TELEPAX: 617-832-7000
STATE:
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LENGTH: 732 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AOMYPLOEIONLTVKLOLOALOONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296
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                  Boston
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                                                         HOAG & ELIOT LLP
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US-08-989-299-8
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NAME: Arnold E., Beth
REGISTRATION NUMBER: 35,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
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LENGTH: 1312 amino acids
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ZIP: 021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 TDEAKADREVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     767 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPEFPKYVEFSNKIAKLNGYTDA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                1116 FDPGSKEHVPANVPYVRYEVSFIIQEQEHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 1175
                                                                                                                                 1056 FLMKMALDKIAFIPFSYLIDQWRWRYFDGSITKENYNQEWWSLRLKYQGLCPPYPRSQGD 1115
                                                                                                                                                                                                                                                                                                                                    877 DGPIPAHLLGNMWAQTWSNIYDLVAPEPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 936
                                                                                                                                                                                                                                                                                                                                                                  259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AOMYPLQEIQNLTVKLQLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
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::|| |:|| |:: : | ||: ::|||:|| || :|: :|| 1133
1176 MKLGYSKPWDEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 1233
                                                                                                                                                                                                                                                                                                   319 GLPNMTQGEWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
                                                                                                                                                                                                 378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                                                  937 GLLPVPPEEWNKSMLEKPTDGREVVCHPSAWDFYNGKDERIKQCTSVNMEDLVIAHHEMG 996
                                                                                                                                                                438 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                             558 LRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSEVGW-STDWSP 612
                                                                                              498 CDPASLEHVSNDYSEIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLENM 557
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nilarity 42.6%; pred. No. 1.2e-118;
Conservative 112; Mismatches 213; Indels 18
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keith E.
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CORRESPONDENCE FOLEY, HOAG & ELIOT LLP
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          650 TDEAKANREVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLOKNKEVSNHTLKYGTW 709
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                                                                                                                                                                                                                                                                                                                          710 AKTEDVSNEQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG-- 767
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                                                                                                                                                                                                                                                           768 TCLSLEPDLTNIMATSRKYBELLWYWKSWRDKYGRAILPEFPKYYDFSNKIAKLNGYSDA 827
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                                                                                                                              878 DGPIPAHLLGNMWAQTWSNIYDLVAPEPSAPSIDATEAMIKQGWTPRRIFKEADNFFTSL 937
                                                                                                                                                             259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                             828 GDSWRSSYESDDLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 877
                                                                                                                                                                                                                           200 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                                                                                                                                                                                                                                                        80 AQMYPLQEIQNLTVKLQLQALQQNGSSYLSEDKSKRLNTILNIMSTIYSTGKVCNPDNPQ 139
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                              378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                938 GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG 997
                                                                                            319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
30.5%; Score 1310; DB 4; Length 1313; atch similarity 42.0%; Pred. No. 2.3e-116; 251; Conservative 115; Mismatches 214; Indels 18; Gaps
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IBM PC compatible
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                  TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                     136 NLPLAKROQYNSLLSNMSQIYSTGKYCFPNKTASCWSLDDDLNNILASSRSYAMLLFAWE 195
                                                                                     107 VLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWE 166
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                                                                                                                                   81 TAENARRQEE-----EALLSQEFAEAWGKKAKELYDPVWQNFTDPELRRIIGAVRTLGPA 135
                                                                                                                                                                  55 TEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEI-----QNLT---VKLQLQALQQNGSS 106
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      21 LLLLLRPPPAALTLDPGLLPGDFAADEAGARLFASSYNSSAEQVLFRSTAASWAHDTNI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 11-DEC-19
                                                                                                                                                                                                                                     7 LLLSLVAVTAAQSTI-------EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
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APPLICANT: RObinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arnold E., Beth
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1177 MKLGYSKOWPEAMKIITGQPNMSASAIMNYFKPLTEWLVTENRRHGETLGWPEYTWTP 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109-2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
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                                                                                                                                                                                                                                                                          h 29.9%; Score 1283.5; DB 4; Length 1310; Similarity 36.8%; Pred. No. 8.2e-114; 75; Conservative 135; Mismatches 262; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                        Indels 75; Gaps
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
APPLICANT: RObinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08989299 Patent No. 6194556
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                                             REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                  NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                   FILING DATE:
                                                                                                                                                           APPLICATION NUMBER: US/08/989,299
                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 LDYFQPVTQWLQEQNERNGEVLGWPEYQWRPPLPNNYPEGIDLVTDEAEASRFVEEYDRS 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 LNYFEPLETWIKDONKNS--FVGW-STDWSPYADOSIKVRISLKSALG------DKA 632
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MOLECULE TYPE: protein US-08-989-299-6
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LENGTH: 737 amino acids
TYPE: amino acid
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US-08-989-299-11
                                                                                                                                                                                           sequence 11, Application US/08989299 patent No. 6194556
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                                                                                                                                               GENERAL INFORMATION:
GRAPPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
APPLICANT: Robinson, Mactomens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DERILMCTKVTMD 367
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                                                                                                                                                                                                                                                                                                                                                                                                                           532 CPPAPRSQGDEDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS 591
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                                                                                                                                                                                                                                                                                                                                                            592 KEAGKRLADAMKLGYSKPWPEAMKVITGOPNMSASAMMNYFKPLMDWLLTENGRHGEKLG 651
                                                                                                                                                                                                                                                                                                                                                                                           548 TEAGOKLENMLRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDON--KNSFVG 605
                                                                                           TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR NUMBER OF SEQUENCES: 14
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                                                                             CORRESPONDENCE ADDRESS:
            STATE:
                                 CITY: Boston
                                                   STREET:
                                                                ADDRESSEE:
COUNTRY:
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One Post Office Square
       USA
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MOLECULE TYPE: protein US-08-989-299-11
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Best Local Similarity
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COMPUTER READABLE FORM:
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CURRENT APPLICATION DATA:
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TELEPHONE: 617-832-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Arnold E., Beth
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 STGKYCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEBYVVL 186
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                                                                                                                                                                                                                                                                                                                                                                                                            187 KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                  188 NTKAAKLNNFTSGAEAWLDEYE-----DDTFEQQLEDI---FADIRPLYQQIHGYVRF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ELAKFMKEVASDTTKFOWRSYOSEDLKROFKALTKLGYAALPEDDYAELLDTLSAMESNF 127
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                                                                                                                                                                                                                                                                                                                              238 RLRKHYGDAVVSETGPIPMHLLGNWWAQQWSEIADIVSPEPEKPLVDVSAEMEKQAYTPL 297
                                                                                                                                                                                                                                                                                                                                                        247 KLMNAY-PSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ 305
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                                                                                                                                                                                                                                                                          298 KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV 357
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                                                                                                                                                                                                                                              365 TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424
                                                                                                                                                              358 TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL 417
                                                                                                                                                                                        425 SPDFQEDNETEINFILKQALTIVGTLPETYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484
                                                    537 LDNCDIYGSARAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE 596
                                                                              539 LHKCDISNSTEAGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYEEPLFTWLKDQ 598
                                                                                                           477 SGIEPPVVRSEKDFDAPAKTHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP 536
                                                                                                                                  485 VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYOFOFQEALC-QAAKH-----EGP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109-2170
                           599 N--KNSFVGWST 608
597 NIKNNVHIGWTT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224; Conservative 122; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 1090; DB 4; Length 615; 36.6%; Pred. No. 9e-96;
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US-08-989-299-12
                                                     RESULT 12
Sequence 12, Application US/08989299
Patent No. 6194556
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LENGTH: 694

TYPE: PRT
ORGANISM: Homo sapiens
                                                                  574 LL--ALKIGSSKPWPEVLKMLTGESEVSTNVFMTYFKPLLTWL 614
                                                                                               553 KLENMLRIGKSEPWTLALENVVGAKNMNVRPILNYFEPLFTWL 595
                                                                                                               514 SEEDFDPGAKFHFSAGVPYÍRRYFLSLVLQFQFHETLCKASGHMGPLHQCDIYNSKIAGK 573
                                                                                                                                           494 DETYCDPASLEHVSNDYSEI-RYYTRTLYQEQEQEALCQAAKHEGPLHKCDISNSTEAGQ 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
23.1%; Score 990; DB 4; Length 694;
Best Local Similarity 37.9%; Pred. No. 4.5e-86;
Matches 221; Conservative 104; Mismatches 228; Indels 30; Gaps
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Sequence 1, Application US/09440325A

Patent No. 6280994
                                                                                                                                                                      454 EVNELMHTALEKTAFTFFGYLMDLFRWKVFDGTTWKDIYNQEWWNLRRLKYOGLCPATPH 513
                                                                                                                                                                                            435 EINFLLKOALTIVGTLPFTYMLEKWRWMVFKGEIPKDOWMKKWWEMKR-EIVGVVEPVPH 493
                                                                                                                                                                                                                              399 EMGHFQYFLQYKNLSIIFRTGANPAFEEAVGSVITLSASSHKHLLNIGLLS--LLED--- 453
                                                                                                                                                                                                                                                  375 EMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNET 434
                                                                                                                                                                                                                                                                                    339 LGLALPPAPPSEWKKLMLMRPTDGREVECHISAWNFYQDDDFRIKKCAEVTTEDPLSIFH 398
                                                                                                                                                                                                                                                                                                               318 VG--LPNMTQGEWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKVTMDDFLTAHH 374
                                                                                                                                                                                                                                                                                                                                           279 GPIPAHLLGENTLAQSWVNILDPVLPFLKKIPEDVTKINKVQHWKPEKLMLEBAETFFTY 338
                                                                                                                                                                                                                                                                                                                                                                     260 GCLPAHLIGD-MWGREWTNLYSLTVPEGQKPNIDVTDAWVDQAWDAQRI-FKEAEKEFVS 317
                                                                                                                                                                                                                                                                                                                                                                                                 229 ALWHSKYESDTLE-----QDLERLFQELRPLYLNPHTYVRRALHRHYGPELIDLR 278
                                                                                                                                                                                                                                                                                                                                                                                                                          201 DYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 LSLESEL-EVMATSRDKEELLWAWQGWQDAVGRQICTTFEHYVELSNKAAQLNGVXKDMG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O. TITLE OF INVENTION: Zac1: A FILE REFERENCE: 98-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYYVLKNEMARANH-YEDYG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/440,325A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 LFKVTQFKDPDVNGMLSKLQNIDKAALSKDELREYNELLAXLEMTYSMAQVCLNEGP--C 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 MYPLOEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQEC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 ETETKIFLQFYDQTGEVVLNKFMEATWNYVTNITRKNQEEMMKDMER-SQFMIYFGTQAH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps
571 TNPHYLYSQKLYPSEHLDIKDSVIINKLYKESLESFTKLPFTIAADNWRYELFDGTYPKN 630
                           413 ATPKHLKSIGLLSPDFQEDNETE-INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKD 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                       511 PNDERVKACAQLGEPDFEQAHSLLVQTYYQYLYKDQSLLFREQASPVITDAIANAFAHLS 570
                                                                                     353 KGDERILMCTKVTMDDELTAHHEMGHIQYDMAYAAQPELLRNGANEGEHEAVGEIMSLSA 412
                                                                                                                452 SAFNTONYTTKKMEVTAYRYFKSAGFPHLPKSYWTSSIFARVWS-KDMICHPAAALDMRA 510
                                                                                                                                 299 D----QAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHP-TAWDL-G 352
                                                                                                                                                                          394 HÁYMRRQLAGTYSNÞYGLSKDGÞÍÞAHLFGSLDGGDWSAHYEQTKPFEEES--ETPEAML 451
                                                                                                                                                                                                     241 HAYVRAKLMNAY--PSYISDIGCLPAHLLGDMWGRFWTNLYSLTVPFFGQKPNIDVTDAMV 298
                                                                                                                                                                                                                                   337 NIITISNEGAKLNGFANGGAMWRSAFDMSSKVHKAEF---DLNKQIDKIYSTIQPFYQLL 393
                                                                                                                                                                                                                                                             182 EYVVLKNEMARANHYEDYGDYWRGDYEVNG-VDGYDYSRGOLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                                                                                                                                                            278 ALNRDSKDSTICDKDVPPPCALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      122 TMSTIYSTGKVCNPDNPQECLLLEDGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                                                                                                                                  218 LDEAENVLTMEVRSTSMQAKQEDMASVTDEKVMRQLGYVSFEGMSALAPSREADYSQAQA 277
                                                                                                                                                                                                                                                                                                                                                                                                           160 SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA 217
                                                                                                                                                                                                                                                                                                                                                                              62 MNNAGDKWSAFLKEOSTLAOMYPLQEIQNLTVKLOLOALQONGSSVLSEDKSKRLNTILN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SSSSWLLLS,VAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Arnold E., Beth
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 11-DEC
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STREET:
STREET:
Boston
MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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N: 514
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US-08-645-193B-15
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                                                                                                                                                                                                                                                          Matches 153;
                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/08645193B Patent No. 5962253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single TOPOLOGY: not relevant MOLECULE TYPE: protein
                               409 NDVKNLEK-NNTVSKINA---
                                                   111 DKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                       384 SNNI-----YLLAIQNNSHIEITE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                              324 ISEAAYILWILSPNHFGTKTIRNYHEFFMDKYGFEQLVNLKQILSDINGFGYPKKDSYSF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                         51 NTNITEENVONMNNAGDKWSAFLKEOSTLAOMYPLOEIONLTVKLOLOALOONGSSVLSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kupke, APPLICANT: Gotz, F
                                                                                                                                                                                                  1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
                                                                                                                                                                                                                                                                  Match 2.9%; Score 124; DB 2 Local Similarity 18.2%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 13-MA
CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 PLLEYYEPLINWLRNTNEIDQVVVGWDGEGTPFTVEEI 777
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 PLLNYFEPLFTWLKDQNK--NSFYGWSTDWSPYADQSI 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631 KLNDRWWEIRNKYEGVRSPQPYNTSNLD--ALIHNSVSQVHS---PATRTLISYVLKFQI 685
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                                                                                                                                                                                                                                                                                                                                                                                                                  990 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202)
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                 -----PVSTEI-----YSEIYF----- 437
                                                                                                                                                                                                                                                                             DB 2; Length 990;
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                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-392-625-20
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                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, (
STREET: 1100 New York Avenue
                                                         APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           887 LYRSND-----TREY------KNLLAKL-----TNPKND 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632 AYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 NVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  856 FIVA---ISIDFLLDYLE---------------INKSEKEEILINNA--ED 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 DYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFFMYDSLL--SINIIQSE-FKIPKE 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 KWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYY- 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708 KEQSFIIPKNRNKHENNLKDWFSIHLSIPKTYQD----NFIQDYLLPFITELKVNNFIN 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 --LSAATPK-----HLK---SIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLE 457
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                                                                                                                                                                                                                Gtz, Friedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
Rosenstein, Ralf
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                                                                                                                                                                                                      Kaletta, Cortina
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             Kessler, Goldstein & Fox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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LENGTH: 990 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 NDVKNLEK-NNTVSKINA------ 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Esmond, Robert W. REGISTRATION NUMBER: 32. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                             532 IDINDIFIGATENKLYLYSEKHDSRIVFVSNSMENYEFGSELYKELREISFEKTKFIQPI 591
                                                                                                                                                                                                                                                                                                                                                                     291 IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQG-----FWENSMLTDPG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPN 290
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                                                                                                                                                                                                                                                                                      338 N-----VQKAVCHPTAWDLGK-----
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                                                                                                                                                                                                       355 DERILMCTKVTMDDELTAHH------EMGHIQYDMAYAAQPELLRNGANEGFHEAVG 405
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                                                                              695 EIVTPLYKKTSLKEQSFIIPKNRNKHFNNLKDWFSIHLSIPKTYQD-----NFIQDYLLP 749
                                                                                                                      406 EIMS-----LSAATPK-----HLK---SIGLLSPDFQEDNETEINFLLKQALT 445
                                                                                                                                                                652 DNRLLL-----NLLNDKHLIILKKELKKHGRIR-----ILESFINESNNERML 694
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750 FITELKVNNFINKFFYIKFKED---EDFIK--LRLLRE------DEDY----- 786
                                       446 IVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             787 -SQIYSFIKNWKDYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFF-MYDSLLDSIN 844
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                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Keliner, Roland
TITLE OF INVENTION: Biosynthetic process for the Preparation
TITLE OF INVENTION: Chemical Compounds
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                              APPLICATION NUMBER: US 07/876,791 FILING DATE: 30-APR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                             FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 22-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                 NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20, Application US/08466961A
3. 5843709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wieland,
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                                                                                                       UMBER: US 07/784,234
31-OCT-1991
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958 CN----RIFGINP 966
                              717 LNDNSLEFLGIQP 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.8%; Score 120; DB 2; Length 990; Best Local Similarity 17.8%; Pred. No. 0.031; Matches 152; Conservative 121; Mismatches 246; Indels 334; Gaps
                                            904 -----TNPKNDYEILKKEFPNLHEFLFNKISILENLKKTLOKSLYTSRSRIIGSFIHMR 957
                                                                                                          877 EEILINNA--EDLYRSND------IREY-----KNLLAKL 903
                                                                          680 SFNFFVTAPKNVSDIIP-----RTEVEKAIRMSRSRINDAF---R 716
                                                                                                                                         620 VRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNOMILFGEEDVRVANLKPRI 679
                                                                                                                                                                           560 LGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIK 619
                                                                                                                                                                                                                                         787 - SQIYSFIKNWKDYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFF-MYDSLLDSIN 844
                                                                                                                                                                                                                                                                         506 VSNDYSFIRYY-----TRTLYQFQFQEALCQAAKHEGPLHKGDISNSTEAGQKLENMLR 559
                                                                                                                                                                                                                                                                                                         750 FITELKVNNETNKEFYIKEKED---EDETK--LRLLRE------DEDY------ 786
                                                                                                                                                                                                                                                                                                                                         446 IVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH 505
                                                                                                                                                                                                                                                                                                                                                                         695 EIVTPLYKKTSLKEQSFIIPKNRNKHENNLKDWESIHLSIPKTYQD-----NFIQDYLLP 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         406 EIMS-----LSAATPK------HLK---SIGLLSPDFGEDNETEINFLLKQALT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                         652 DNRLLL-----NLLNDKHLIILKKELKKHGRIR-----ILESFINESNNERML 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 DERILMCTKVTMDDFLTAHH-----EMGHIQYDMAYAAQDFLLRNGANEGFHEAVG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 TEEGIDSLPEGPRIIYKNIILKPATWKINSEMESETENWLNREATIRKWHIPKDVIIAFG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 IDINDIFIGATFNKLYLYSEKHDSRIVFVSNSMFNYEFGSELYKFLREISFEKTKFIQPI 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 IDVTDAMVDQAWDAQRIFKB---AEKFFYSVGLPNMTQG-----FWENSMLTDPG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 -----HYNNYMNENDLEISQLNEAPLNSRNVNILNN--NRIYNTCLNLNLP----KSD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 BEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 --GNSIKG-YEDFAVISPILGSFNAGATFGRP-TGNFNIK-----KKNQLQKEIVH-- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 EVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 NDVKNLEK-NNTVSKINA------ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 DKSKRLNTILNTMSTTYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 SNNI-----AFLKEK-----AFLKEK-------YLLAIQNNSHIEITE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 ISEAAYILWLLSPHEEGTKTIRNYHEFFMDKYGFEQLVNLKQLLSDINGFGYPKKDSYSF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 NTNITEENVONMNNAGDKWSAFLKEQSTLAOMYPLOEIQNLTVKLOLOALOONGSSVLSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 683 amino acids
322 NMTQGFWENSMLTDPGNVQKAVCH----PTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378
                               273 WEKRVDSTDRVYEVNHNTKTTQWEDPRTQGLQNEEPLPEGWEI-RYTREGVRYFVDHNTR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46,
Patent No. 6
                                                              227 EHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFG 286
                                                                                                                                                          191 -----POPLPPGWERRVDDRRRVYYVDHNTRTTTWQRPTMESVRNFEQWQSQRNQL---- 241
                                                                                                                                                                                       168 WRSEVGKOLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYE-VNGVDGYDYSRGOLIEDV 226
                                                                                                                                                                                                                      135 FEAAKSROPDGCMDPVRQQSG----NANTETLPSGWEQRKDPHGRTYYVDHNTRTTTWER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                     127 YSTGKVCNPDNPQECLLLEPGLNEIMANS------LDYNERLWAWES 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     86 -----STTVEDPPVQEILTSSENNECIPSTSAELESEARSILEPDTSN------SRSSSA 134
                                                                                                                                                                                                                                                                                                                72 FLKEQSTLAQMYPLQEI-----ONLTVKLQLQALQONGSSVLSEDKSKRLNTILNTHSTI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   44 LASEPADDTVNGESSSFAPTDN------ASVTGTPVVSEENALSPNCT----- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                  12 VAVTAAQSTIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pirozzi, Gregoric
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MISROCK, S. LESLIE REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 03-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 116.5; DE 18.0%; Pred. No. 0.036;
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|--|-------------------|-------------------|---|----|----|-------------------------------|--|--|----|-----------------|----|------|--------------------------------------|-----------|------------------------------------|--|
| US-08-844-059-2 US-08-844-059-2 Sequence 2, Application US/08844059 Patent No. 6001601 Patent No. 6001601 Patent No. 6001601 GENERAL INFORMATION: No. 6001601el Compounds TITLE OF INFORMATION: ADDRESSEE: Smithkline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Frussia STREET: PA COUNTRY: USA ZIF: 19046 ZIF: 19046 ZIF: 19046 ZIF: 19046 ZIF: 19046 COMPUTER READABLE FORM: REDINT THE SYSTEM: DOS OPERATING SYSTEM: DOS OPERATION NUMBER: US/08/844,059 PILING DATE: 18 ADR-1999 APPLICATION NUMBER: 9607999.1 PILING DATE: 18 ADR-1999 APPLICATION NUMBER: 9607999.1 PILING DATE: 16 ADR-1999 APPLICATION NUMBER: 38,891 REGISTRATION UMBER: 38,891 REGISTRATION UMBER: 931456 REFERENCE//DOCKET NUMBER: 931456 REFERENCE//DOCKET NUMBER: 931456 REFERENCE//DOCKET NUMBER: 38,891 REGISTRATION UMBER: 9307999.1 PILING DATE: 16 10-270-4078 TELEGRAM: 610-270-4078 TELEGRAM | 649 TDNEVRMRL 657 | 698 TEVEKAIRM 706 | 595VPLQWLQYFDEKELEVMLCGMQEVDLADWQRNTVYKHYTKNSNV1-WIWX | | | PYADUSIKYRISEKSALGUKAFIDGFNEV | 503 TIKDLESIDTEEYNSLIWIRDNNLEECGLEMIESVEWILTEGATGDKAYEWNDNEM 640 | SNOTE STATE OF THE | | - PHUELIC STILL | | | FAL TO AT THE VOTE DETYMLEKWRWMVFKGE | | 332 TTTFKDPRNGKSSVTKGGFQ LAIENG FA | TOTAL TRANSPORT OF THE PROPERTY OF THE PROPERT |
| Db Qy Qy Db Qy Qy Db Qy Db | 7 V | фф | Qy | Db | Qγ | фd | Qy | Дb | Qy | DЬ | VΩ | dd | Qy | Mato | Quer | us-08- |

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2.6%; Score 113.5; DB 3; Length 665;
st Local Similarity 19.2%; Pred. No. 0.067;
tches 135; Conservative 99; Mismatches 231; Indels 239; Gaps
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                                                                                                                                                        Sequence 2, Application US/09431202 Patent No. 6294175
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                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 -SGWYSVS--DEEFFTESQLAEVFRDEAGNVTGGIAPSGHEVEWVSEESYFLRLSKYQDR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LVEFFKAHPEFITPDGRLNEMLRNFIEPGLEDLAVSRTTFTWGVPVPSNPKHVVYVWIDA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 LLDISYDKFIRTIDDYHEKVVA------QVFERLLAQDDIY--LGEY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GWFVMKDGKMSKSKGNVVYPEMLVERYGLDPLRYYLMRNLPVGSDGTFTPEDYVGRINYE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LLNYATALGYAODEHGNEDKFWNGTVFHMVGKDILREHSIYWPILLMMLDVKLPDRLIAH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 MAYAAQPELLR-----NGANEGFHEAVGEIMSLSAATPKHLKSTGLLSPDFQEDNE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 A-VDY--PRALEAVWTLISRTNKYIDETAPWVLDKDEALRDQLASVMSHWQASIRVVAHL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 TEINELLKOALTIVGTL---PETYMLEKWRWMVFKGEIPKDQW---MKKWWEMKREIVGV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 LANDLGNILLNRTVSMINKYFDGQIPAYVEGVTEFDHVLAEVAE--KSIA----DFHTHME 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 TEAGOKLENMLRLGKSEPWTLALENV-----VGAKNMNVRPLLNYFEPLFTWLKD 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 -----LTQIGLEE--VSSLENLSLADFPADVTVVAKGTPIFPRLNMEEEI-AYIKE 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 QNKNGEVGWSTDWSP------YAD-QSIKVRIS-----LKSALGDKAYEW--- 635
                                                                                           APPLICANT: Lawlor, Elizabeth TITLE OF INVENTION: No. 62941
                                                                                                                                                                                                                                                                                                                                                                                                  636 -NDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDI 694
                                                                                                                                                                                                                                                                                                                                                                                                                                       532 QMEGNKPAVEKEWNPDEVELKLNKDEIKFEDFDKVEIRVAEVKEVSKVEGSDKLLQFRLD 591
                                                          CORRESPONDENCE ADDRESS:
                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                               629 ------KMMKKYVSQGMILSAEHDGKLTLLTVDPAV--PN 660
                                                                                                                                                                                                                                                                                                                    695 IPRTEVEKAIRMSRSRINDAFRL---NDNSLEFLGTQPTLGPPN 735
                                                                                                                                                                                                                                                                                                                                                           592 AGDGEDRQILSGIA----KYY---PNEQELVGKKVQIVANLKPR-----
CITY: King of Prussia
                                         ADDRESSEE:
                       709 Swedeland Road
                                           SmithKline Beecham Corporation
                                                                                    No. 6294175el Compounds 6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett

Diskette

COMPUTER: IBM Compatible

COUNTRY: STATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-09-431-202-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.6%; Score 113.5; DB 4; Length 665; Best Local Similarity 19.2%; Pred. No. 0.067; Matches 135; Conservative 99; Mismatches 231; Indels 239; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 9314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 amino acid
592 AGDGEDRQILSGIA----KYY---PNEQELVGKKVQIVANLKPR----------
                                   636 - NDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDI 694
                                                                              532 QMEGNKPAVEKEWNPDEVELKLNKDEIKFEDFDKVEIRVAEVKEVSKVEGSDKLLQFRLD 591
                                                                                                                      598 QNKNSFVGWSTDWSP------YAD-QSIKVRIS----LKSALGDKAYEW--- 635
                                                                                                                                                                 484 -----LTQIGLEE--VSSLENLSLADFPADVTVVAKGTPIFPRLNMEEEI-AYIKE 531
                                                                                                                                                                                                                                                 472 IEP------ 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/844,059
                                                                                                                                                                                                         548 TEAGOKLENMLRIGKSEPWTLALENV------VGAKNMNVRPLLNYFEPLETWLKD 597
                                                                                                                                                                                                                                                                                       488 VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS 547
                                                                                                                                                                                                                                                                                                                                  415 A-VDY--PRALEAVWTLISRTNKYIDETAPWVLDKDEALRDQLASVMSHWQASIRVVAHL 471
                                                                                                                                                                                                                                                                                                                                                                          434 TEINFLLKQALTIVGTL---PFTYMLEKWRWMVFKGEIPKDQW---MKKWWEMKREIVGV 487
                                                                                                                                                                                                                                                                                                                                                                                                                     361 LANDLGNLLNRTVSMINKYFDGQIPAYVEGVTEFDHVLAEVAE--KSIA----DFHTHME 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 MAYAAQPFLLR-----NGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GWFYMKDGKMSKSKGNVYYPEMLVERYGLDPLRYYLMRNLPYGSDGTFTPEDYYGRINYE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 GFW---ENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYD 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LLNYATALGYAQDEHGNFDKFWNGTVFHMVGKDTLRFHSTYWPILLMMLDVKLPDRLIAH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LVEFFKAHPEFITPDGRLNEMLRNFIEPGLEDLAVSRTTFTWGVPVPSNPKHVVYVWIDA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 MV-----FVSVGLDN--MTQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 RAKLMNAYPSYISPIGCLPAHL-----LGDMWGRFWTNLYSLTVPFGQKPNIDV-TDA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 -SGWYSVS--DEEFFTESQLAEVFRDEAGNVTGGIAPSGHEVEWVSEESYFLRLSKYQDR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 WRGDYEVNGVDGYDYSRGQLIE------DVEHTFEEIKPLYEHLHAYV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 LLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 LLDISYDKFIRTTDDYHEKYVA-------QVFERLLAQDDIY--LGEY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 610-270-44; TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/431,202
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| | 213 DGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWG 272 | Qy | |
|-----|---|-------|--|
| | | Db | |
| | 159 NERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGV 212 | Qy | |
| | HGGSQGQLLHPGDHKAQAHNKALPPGLSKEQAPDCSSSDG 62 | В | |
| | 15 | Qy | |
| | AEALFRPG | Db | |
| | 110 E 122 | Qy | |
| | | Db | |
| • | | Qy | |
| 19 | Query Match 2.4%; Score 104; DB 1; Length 834; Best Local Similarity 20.5%; Pred. No. 0.81; Matches 88; Conservative 59; Mismatches 142; Indels 140; Gaps | ¥ # O | |
| | ANTI-SENSE: NO 08-491-357-2 | us- | |
| | MOLECULE TYPE: protein HYPOTHETICAL: NO | | |
| | STRANDEDNESS: not relevant TOPOLOGY: not relevant | ٠. ٠. | |
| | TYPE: amino acid | ٠. ٠ | |
| | SEQUENCE CHARACTERISTICS: | | |
| | TELEFAX: (215) 563-4044 INFORMATION FOR SEC ID NO. 2: | ٠. ٠. | |
| | TELEPHONE: (215) 563-4100 | ٠. ، | |
| | REGISTRATION NUMBER: 36,252 | | |
| | ATTURNEY/AGENT INFORMATION: NAME: Reed, Janet E. | | |
| | CLASSIFICATION: 435 | | |
| | APPLICATION NUMBER: US/08/491,357 | | |
| | SUFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: | ٠. ٠. | |
| | OPERATING SYSTEM: PC-DOS/MS-DOS | • • • | |
| | MEDIUM TYPE: Floppy disk | | |
| | COMPUTER READABLE FORM: | ٠ | |
| | COUNTRY: USA | | |
| | | | |
| | ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 | •• •• | |
| | CE ADDR | ٠ | |
| , i | ALTERATIONS | | |
| TCA | OF INVENTION: | ٠ | |
| | Estojak, Joanne | | |
| | APPLICANT: Golemis, Erica A. APPLICANT: Law. Susan | ٠. ٠. | |
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| | equence 2, | | |
| | SULT 19 -08-491-357-2 | RES | |
| | 629KMMKKYYSQGMILSAEHDGKLTLLTVDPAVPN 660 | Db | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08968633
Patent No. 6100384
                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Law, Susan
APPLICANT: Estojak, JOAnne
TITLE OF INVENTION: MCLEIC
TITLE OF INVENTION: MEDIATC
TITLE OF INVENTION: ALTERAT
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 TQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDF--LTAHHEMGHIQY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 QCETHFISL-----LNAIDALFSCVSSAQPPRIFVAHSKFVILSAHKLVFIG-DTL 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 REWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ--RIFKEAEKF-----FVSVGLPNM 323
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       816 DLSRNAQLF 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 DMAYAAQPF 390
                                     442 ERHINEIRTAVDKVELFLKEYLHFVKGAVANAACLPELILHNKMKRELQRV-EDSHQILS 500
   110 E-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: No. 6100384 Relevant
TOPOLOGY: No. 6100384 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/968,633 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                          56 EENVQNMNNAGDKWSAFLKE-----QSTLAQMYPLQE-IQNLTVKLQLQALQQNGSSVLS 109
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LSQFQLLEQ-----EITKPVENDISKW----KPSQSLPTTNSGVSAQDRQLLCFYYD 713
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                                                                                                                    88;
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1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                           834 amino acids
                                                                                                                                                                                                                                                                                                                                                                                (215) 563-4100
(215) 563-4044
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                                                                                                                  Conservative
                                                                                                                                                                                                                 NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            : protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERATIONS
                                                                                                                                  2.4%; Score 104; DB 3; Length 834; 20.5%; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/491,357
                                                                                                                    59; Mismatches 142; Indels 140;
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         --DKSKRLNTILNT----- 122
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Search completed: March 13, 2003, 16:58:30 Job time : 29 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 -----MSTIY----STGKVCNP-DNPQEC--LLLEPGLNEIMA---NSLDY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 QTSHDLNECSWSLNILAINKPQNKCDDLDREVMVAKTVPDDAKQLTTTINTNAEALERPG 560
                                                                                                                                                                                                                                                                                                                                                                                                    666 ----LSQFQLLEQ-----EITKPVENDISKW---KPSQSLPTTNSGVSAQDRQLLCFYYD 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 DGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 PGSLHLKNGPESIMNSTEYPHGGSQGQLLHPGDHKAQAHNKALPPGLSKEQAPDCSSSDG 620
                                                                                                                                                                                                764 TRQVTAQDIRNKVMNSSNQLCEQLK-----TIVMATKMAALHYPSTTALQEMVHQVT 815
                                                                                                                                                                                                                                                324 TQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDF--LTAHHEMGHIQY 381
                                                                                                                                                                                                                                                                                                  714 QCETHFISL-----LNAIDALFSCVSSAQPPRIFVAHSKFVILSAHKLVFIG-DTL 763
                                                                                                                                                                                                                                                                                                                                                  273 REWINLYSLIVPEGOKPNIDVTDAMVDQAWDAQ--RIFKEAEKF-----FVSVGLPNM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 SERSWMDDYDYVHLQGKEEFERQQKELLEKENIMKQNKMQLEHHQ------
                                                                                                 816 DISRNAQLE 824
                                                                                                                                                   382 DMAYAAQPF 390
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq length: 0
DB seq length: 2000000000
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result

Query

| 19 | 18 | 17 | 16 | 15 | 14 | ü | 12 | 11 | 10 | 9 | œ | 7 | σ | ъ | 4 | ω | N | ם | No. |
|------------------|-------------------|------------------|-------------------|------------------|------------------|-------------------|------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------|
| 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 2979 | 3561 | 3579 | 3643 | 3775 | 4287 | 4291 | Score |
| 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 83.0 | 83.4 | 84.9 | 88.0 | 99.9 | 100.0 | Match I |
| 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 555 | 805 | 805 | 681 | 711 | 805 | 805 | Length I |
| 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | ဖ | 9 | 9 | ₽B |
| US-10-142-419-72 | US-10-140-002-72 | US-10-143-114-72 | US-10-142-431-72 | US-10-140-474-72 | US-10-137-865-72 | US-10-176-921-72 | US-10-176-918-72 | US-10-175-746-72 | US-10-140-470-72 | US-10-123-904-72 | US-10-121-049-72 | US-10-028-072-72 | US-09-978-385-9 | US-09-978-385-6 | US-09-969-384-25 | US-09-969-384-13 | US-10-114-893-86 | US-09-978-385-2 | ID |
| • | Sequence 72, Appl | • | Sequence 72, Appl | ` | ` | Sequence 72, Appl | • | Sequence 72, Appl | • | • | Sequence 72, Appl | Sequence 72, Appl | Sequence 9, Appli | Sequence 6, Appli | • | Sequence 13, Appl | Sequence 86, Appl | Sequence 2, Appli | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 2 |
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| 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 212 | 694 | 1265 | 107 |
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| 711 | US-10-176-921-482 | US-10-176-918-482 | US-10-175-746-482 | US-09-997-666-387 | US-09-997-428-387 | US-09-990-562-387 | US-09-990-438-387 | US-10-140-470-482 | US-10-123-904-482 | US-10-121-049-482 | US-09-993-667-387 | US-09-997-653-387 | US-10-028-072-482 | US-09-989-734-387 | US-09-993-687-387 | US-09-991-181-387 | US-09-990-436-387 | US-09-989-730-387 | US-09-990-444-387 | US-09-989-735-387 | US-09-989-293A-387 | US-09-992-598-387 | US-09-846-996A-1 | US-09-964-899-19 | C2 405 505 C0 C0 |
| | Sequence 482 | Sequence 482 | Sequence 482 | | Sequence 387 | Sequence 387 | Sequence 387 | Sequence 482 | Sequence 482 | Sequence 482 | Sequence 387 | Sequence 387 | | Sequence 387 | Sequence 387 | | Sequence 387 | Sequence 387 | Sequence 387 | Sequence 387 | | Sequence 387 | Sequence 1, | Sequence 19, | 'cz apmanhae |
| • | • | • | • | • | ` | 7, App | ` | ` | - | - | • | - | • | • | • | • | • | • | , App | • | • | | | Appl | Toldy |

ALIGNMENTS

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; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-385-2
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANY: BISHOP, PAUL D.

TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CUBRENT APPLICATION NUMBER: US/09/978,385.
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/563,516
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APPLICANT: Piddington, Christopher
APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 805; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 2, Application US/09978385
Patent No. US20020177211A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-05-03
61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                  NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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Gaps

Homo sapiens

DB

Length

805;

0

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GENERAL INFORMATION:
APPLICANT: MCCOY, John M.
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
                                                                     APPLICANT: Kelleher, Kerry S.

APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND PORTIE REFERENCE: GI 6000-10A

CURRENT EPILING INTEREST OF THE PROTEINS OF THE P
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US-10-114-893-86
        SEQ ID NO
LENGTH:
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                                                        NUMBER OF SEQ ID NOS: 3: SOFTWARE: PatentIn Ver.
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                  RESULT 3
US-09-969-384-13
IS-09-969-384-13
Sequence 13, Application US/0
Publication No. US20020192740
GENERAL INFORMATION:
APPLICANT: MOORE, et al.
TITLE OF INVENTION: Human G
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; ORGANISM: HO
US-10-114-893-86
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FILE REFERENCE:
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YASIDISKGENNPGFQNTDDVQTSF
                                                            SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
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Pred. No. 0;
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LENGTH: 711
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PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
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CURRENT FILING DATE: 2001-10-03
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LOCATION: (240)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (219)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                 662 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNS 721
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Best Local Similarity
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PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
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PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
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CURRENT FILING DATE: 2001-10-03
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TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (240) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                              GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 481
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                                            TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
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99.3%;
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US-09-978-385-6
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Piddington, Christopher S. APPLICANT: Petrie, Charles APPLICANT: Shoemaker, Kimberly E. APPLICANT: Bishop, Paul D. TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mouse
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301 AWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                181 EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                                                121 NTMSTIYSTGKVCNPKNPQECLLLEPGLDEIMATSTDYNSRLWAWEGWRAEVGKQLRPLY
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                                                                                                                                                                                                                                                                                                                                       1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFUHEAEDLFYQSSLASWUYUTUTTEENVQ 60
                                                                                                              EEYVVLKNEMARANNYNDYGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIKPLYEHL
                                                                                                                                                                                                 NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
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APPLICANT: Piddington, Christopher S.
APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACEZ: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT APPLICATION NUMBER: 60/133,952
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR APPLICATION NUMBER: 60/151,181
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PRIOR APPLICATION NUMBER: 09/563,516
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Patent No. US20020177211A1
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                                                                                                                                                                                                                                                                                                                        LENGTH: 805
TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
61 KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
                              61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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                                                                                                                                                                                                               h 83.0%; Score 3561; DB 9; Length 805; Similarity 81.9%; Pred. No. 1.4e-287;
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                               Sequence 72, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
                                                                                                                        APPLICANT:
              APPLICANT: APPLICANT:
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                             Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K Wood, William
                                                                                         Smith, Victoria
                                                                                                                        Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                          Goddard, Audrey
                                                                                                                                                                       Gerritsen, Mary E
                                                                                                                                                                                                      Filvaroff, Ellen
                                                                                                                                                                                                                                                   Beresini, Maureen
                                                                                                        Sherwood, Steven
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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PRIOR FILING DATE: 1997-09-17
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FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/064809
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APPLICATION NUMBER: 60/073612
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OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/088730

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APPLICATION NUMBER: 60/089907
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KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQFQEALCQAAKHEGPLH
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                                                                                    IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                      CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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APPLICATION NUMBER: 60/088858
                                                                IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                                  AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
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Pred. No. 1.9e-239;
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US-10-121-049-72
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CURRENT FILING DATE: 2002-04-12
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APPLICANT: Beresini, Mauro
APPLICANT: DeForge, Laura
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NUMBER OF SEQ ID NOS: 550
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 1.9e-239;
1; Mismatches 0;
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; TYPE: PRT
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US-10-123-904-72
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Publication No. US20030022328A1
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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Pred. No. 1.9e-239;
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US-10-140-470-72
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APPLICANT: Beresini, Maure,
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
APPLICANT: Gao, Wei-Qiang
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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                     EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
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Zhang, Zemin
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                      Conservative
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99.8%;
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    Mismatches

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LENGTH: 555
TYPE: PRT
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Publication No.
                                                                                                                            Matches
                                                                                                                                                        Query Match
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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APPLICANT:
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NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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                                                                                                                            Conservative
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99.8%;

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                                                                                                                                           Score 2979; DB 9;
Pred. No. 1.9e-239;
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-176-918-72
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APPLICANT: Baker, Kev
APPLICANT: Beresini
APPLICANT: DeForge,
   Query Match
Best Local Similarity
Matches 553; Conserv
                                                                                                          CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILLING DATE: 2002-06-20
Prior Application removed - See File WI
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 72
LENGTH: 555
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APPLICANT:
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Wood, William
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    Conservative
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                   69.4%;
99.8%;
 Score 2979; DB 9;
Pred. No. 1.9e-239;
L; Mismatches 0;
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                              Length 555;
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RESULT 13
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            SEQ ID NO 72
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                                                  APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
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APPLICANT:
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                            Prior Application removed - NUMBER OF SEQ ID NOS: 550
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LENGTH:
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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           TITLE OF
                                       APPLICANT:
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E OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC OF INVENTION: ACIDS ENCODING THE SAME REFERENCE: P3330R1C154
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                                       Zhang, Zemin
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                                                                                                                                       Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                     Watanabe, Colin K
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US-10-140-474-72

Sequence 72, Application US/10140474 Publication No. US20030032156A1 GENERAL INFORMATION:

APPLICANT:

Baker, Kevin P.

Beresini, Maureen

DeForge, Laura Desnoyers, Luc Filvaroff, Ellen

APPLICANT

Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J
Gurney, Austin L.
Sherwood, Steven

Smith, Victoria Stewart, Timoth

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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 72
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CURRENT FILING DATE: 2002-05-03
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ORGANISM: Homo
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            KCDISNSTEAGQKL 554
                                                                   KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                                    KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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Pred. No. 1.9e-239;
1; Mismatches 0;
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RESULT 16
US-10-142-431-72
Sequence 72, Application US/10142431
Publication No. US20030036179A1
GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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LENGTH: 555
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Local Similarity 99.8%;
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RESULT 17
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LENGTH: 555
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CURRENT FILING DATE: 2002-05-10
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Sequence 72, Ap Publication No.

Application US/10143114 No. US20030036180A1

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FILE REFERENCE: P3330R1C211
CURRENT APPLICATION UMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                               KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQEQEALCQAAKHEGPLH
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Watanabe, Colin K
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CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
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Similarity 99.8%;
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Pred. No. 1.9e-239;
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CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper
NUMBER OF SEQ ID NOS: 550
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APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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                         AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
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Godowski, Paul J.
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99.88;
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Pred. No. 1.9e-239;
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; ORGANISM: Homo sapiens
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LENGTH: 261
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Best Local Similarity 99.6%;
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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moore, et al.
TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA
                                                                                             242 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
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241 WDAQRIFKEAEKF 253
                                        302 WDAQRIFKEAEKF 314
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SUMMARIES

Description

Result

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4142 3740.5 3579 3579 3562 3561 3561 3561 2904 2904 2167 1347.5 Score Query Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Length DB 2418 3813 3939 4563 46564 2551 4010 4011 4011 4011 4112 2490 4020 4020 4022 4022 10 9 6 10 10 AX047764) AB053182 BC036375 AF291820 AX047758 AR135177 CHKACEI) AF201331 AR037213 AR137383 AX047762 AX418984 AR135178 A00914 **HSM800880** AB046569 AF241254 AX431513 AX418982 AX147503 OCANCOE AX429555 HUMAICEB AX047760 RNU03708 RNU03734 BC026801 MUSACEA BC034367 MUSACEB MUSACEC AF201332 E43987 ACE-analogo E39033 MPROT15 pol E43988 ACE-analogo AF291820 Homo sapi AX047758 Sequence AR135177 Sequence AB053182 Mus muscu BC036375 Homo sapi BC034367 Mus muscu M26657 Human testi X16295 Human mRNA A31567 H.sapiens t BC026801 Mus muscu AB053181 Mus muscu AX047765 Sequence AX047760 Sequence AX047764 Sequence AB046569 Homo sapi ALI10224 Homo sapi AX463938 Sequence E39034 MPROT15 pol AX047762 Sequence J04947 Mouse angio M29981 Human aberr L40175 Gallus gall AF201331 Rattus no AF201332 Rattus no U03708 Rattus norv U03734 Rattus norv M26658 Human testi X62551 O.cuniculus AR135178 Sequence AX418984 Sequence AF241254 Homo sapi AX431513 Sequence AX418982 Sequence AR037213 Sequence AR137383 Sequence AX147531 Sequence AX147503 Sequence AX429555 Sequence A00914 H.sapiens 9 J04144 Human angio J04946 Mouse angio M55333 Mouse testi

ALIGNMENTS

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| OURCE Unknown. ORGANISM Unknown. Unclassified. Unclassified. Unclassified. Unclassified. I (bases 1 to 2415) AUTHORS Acton, S. Laurene. and Robison, K. Earl. Angiotensin converting enzyme homolog and therapeutic and diagnostic uses therfor JOURNAL Patent: US 6194556-A 3 27-FEB-2001; EATURES SOURCE Organism="unknown" ASE COUNT 743 a 483 c 555 g 634 t | SOUR REFE AU TT JOI FEATI |
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                                                                                                  Angiotensin converting enzyme homolog and Patent: WO 0212471-A 3 14-FEB-2002; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 3 from Patent WO0212471.
AX418984
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                      GCCTGGGATGCACAGAGATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT
                                   AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu
                                                                    TIGACAGITCCCTTIGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG
                                                                                 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln
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PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
                  CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC
                             GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
                                                        TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAAGTAAAAAAT 1980
                                                                  TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn
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Query Match:
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Sugano, S. and Komatsu, T.
ACE-analogous gene
Patent: JP 2001046072-A 1 20
OTSUKA PHARMACEUT CO LTD
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A61K39/395, PC A61K39/395,
PC A61K39/395, A61K48/00, A61P9/12, C07K14/47, C07K16/08, C12N1/15,
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| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis 1081 TGCACAAAGGTGACAATGGACGATTTCTGCTGACAGCTCATCAGAAGTGGACAAT 381 TyrAspMetAlaTyrAlaAlaGlpropheLeuLeuArgAsnGLyAlaAsnGl 381 TyrAspMetAlaTyrAlaAlaGlpropheLeuLeuArgAsnGLyAlaAsnGl 141 TATGGTATTGGCTATTGCTGCTAAGAATGAGCCACTATGAAATGGACTATTGATATGATTGGACTATTGATATGATTGGACTATTGATAGATTGACTATTGATAAATGATGACTATTGATAAATGATTGACTATTGATATGATTGACATTTCTGCTAAGAAATGAACCATTTCAGAAATGAAATGAACCATTTAAAATGAATG | 81 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThr | N | |
| 361 CysThriysValThrwetAspAspPheLeuThrAlaHiSHiSGluMetGlyHiSI | 161 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgI | H | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisI | 41 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysVall | — | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGlumetGlyHisIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 21 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnC | ₽ | |
| 1081 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATGATAAGATGACAATGGACAATGCACAAAGGTGACAATGGACAACTTCCTGACAGCTCATCATGAGAATGGACAGCTGACAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGTGACAAAGGAAATGAAAAGAAATGGACATGAAATGAAAAGAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAATGAAAATTAAACATTCAAAAAAAA | 01 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIle | | |
| 1361 CYSThrLySValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis | 81 ValargProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnA | ₽ . | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisJ | 61 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnM | ш | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisJ | 41 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuA | 1 | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis | 21 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyPro | 1 | |
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| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisJ | 81 LysargGluIleValGlyValValGluProValProHisAspGluThrTyrCys | L) | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisJ | 61 TrpMetVa1PheLysG1yG1uIleProLysAspG1nTrpMetLysLysTrpTrpG | . 🚨 | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisJ | 41 LysGlnAlaLeuThrIlevalGlyThrLeuProPheThrTyrMetLeuGluLysT | ⊢ | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis1 | 21 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLe | ⊢ | |
| 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis1 | 01 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuL | 1 | |
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

E 1 (bases 1 to 2418)

S Christopher, D. S. and Micola, B.

MPROT15 polypeptide and MPROT15 polynucleotide

Pattent: JF 199318472-A 1 24-NOV-1999;

SMITHKLINE BEECHAM CORP PUBLIC LTD CO

OS Homo sapiens (human)

PN JF 199318472-A/1

PD 24-NOV-1999

PF 22-JAN-1999 JF 1999014949

PF 22-JAN-1999 GB 9810373:2,18-AUG-1998 GB

CHRISTOPHER D SAZAN, MICOLA BAGESU

PC C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31

PC A61K39/00,

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FH Key Location/Qualifiers

FT SOURCE 1.2418

/Organism-'Homo sapiens (human)
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 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu
                            SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
                                                                                     GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC
                                                                                                                {\tt GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn}
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                                               IleGluGluGluAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe
TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
                                   ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC
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A61K37/64,
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patent: JP 2001046072-A 2 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
OS Unknown
PN JP 2001046072-A/2
PD 20-FEB-2001
PF 06-AUG-1999 JP 1999223892
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Sugano, S. and Komatsu, T.
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C12N15/09, A61K31/00, A61K31/7088, A61K38/00, A61K38/55,
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Submitted (01-AUG-2000
Pharmaceuticals, Inc,
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Donoghue, M., Woolf, B., Robison, K.
Direct Submission
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Donoghue, M., Hsieh, F., Baronas, E., (Stagliano, N., Donovan, M., Woolf, B.,
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Mammalia; Eutheria;
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RGSSVLSEDKKSKRLNTILNTMSTIYSTGKVCNPDNPGECLLLEPGLNEIMANSLDYNE
RLWAWESWRSEVGKQLRPLYEEVYVLKEMARANLYBYIGTDYDYNGYDGYDYS
RGOLIEDVEHTFEEIKPLYEHLHAYVDAKLANAYPSYISPIGCLPAHLLGDMWGRFWT
NLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFVSVGLPNHYGGYENSMLTI
NLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFTVSVGLPNHYGGFWENSMLTI
DPGNNVQKAVCHPTAWDLGKGDFRLIMCTKVTWDDELTAHHEMGHIQYDMAYAAQPFLL
RNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSDPGCDDNETEINFLLKQALTIVGTL
PFTYMLEKWRWAVFKGEIFKDQMKKWWEMKREIVGYVEPVPHDETYCDAASLFHVSH
USSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPW
TLALENVGAKMNVRFPLLNTFEPLFTWLKDQNKUSFVGWSTDWSFYADQSIKVRISL
TALENVGAKMNVRFPLLNTFEPLFTWLKDQNKUSFVGWSTDWSFYADQSIKVRISL
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                                                                                                                                                                                                                                                                                                                                                                                                    /product="ACE-related carboxypeptidase ACE2"
/protein_id="AAF99721.1"
/db_xref="GI:9802433"
/translation="MSSSSWLLLSLYAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (01-AUG-2000) Cardiovascular Biology, Miticals, Inc. 75 Sidney Street, Cambridge,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 3334)
Piddington, C.S., Petrie, C.R., Shoemaker, K.E. and Bish
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Patent: WO 0070032-A 1 23-NOV-2000;
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DYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFYNNLRLGKSEPW
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KSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNOMILFGEEDVRVANLKERISFN
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RLMAMESWRSEVGKQLRPLYEEYVVLKNEMARANYSDYGDYNEGDYEVNGVDGYDYS
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IWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFQNT
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| 400 | . Tyr $\mathtt{AspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe}$ | 381 | Qy |
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| 1174 | TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG | 1115 | В |
| 380 | ysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln | 361 | Оу |
| 360 1114 | APARGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAACGCCGACTTCAGGATCCTTATG | 1055 | Dp 4 |
| 0 | CLIAALATGACICAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG | ٠ ر | |
| 4 | ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | 321 | } Q |
| 994 | GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT | | 말 |
| 320 | AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu | 301 | οy |
| w | TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG | 875 | 문 |
| Ö | . LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln | 281 | Q |
| 280 874 | CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer | 261 815 | Фр |
| 814 | CATECCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTTGGA | 755 | Db |
| 260 | HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly | 241 | Qy |
| | | 9 | DЪ |
| 240 | GlnLeuIleGluAspValGluHisThrPheGluGluIleLvsProLeuTvrGluHisLeu | 2 | Qy |
| Ñ | - ASPLYLLEAGUS ASPLYTGLIVALASDGLYYALASDGLYTYRASPTYRSERARGGLY - | | B 5 |
| ū | ACOMINATES TO THE TRANSPORT OF THE TRANS | ٠ - | |
| 0 | 1 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly | 18: 57: | Db Qy |
| 574 | 5 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT | \vdash | ф |
| 180 | rgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr | | Qy |
| 1 | 5 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG | 5 | Db |
| | ysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGl | | Qy |
| G | | 9 | ф |
| 4 | .nThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlr | N | Qγ |
| 394 | | | Db |
| o | lnGlnAsnGlvSerSerValLeuSerGluAspLvsSerTvsArgTenAsnThrTle | | Qy |
| ω | | | ДD |
| | lnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLe | œ | Qy |
| | ACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC | | Db |
| 0 | .snMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAl | 0 | Qy |
| 60 214 | TyroinSerSerLeuAlaSerTrpAspTyrAspThzhapileThrGluGluAspValGln | 15 | Db 03 |
| 154 | MII GAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTT | | , 5 |
| 40 | 1 11eGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe | | |
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| 760 | 11 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 7 | γ 74 | Qy |
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| 2254 | 95 AGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 2 | b 219 | 맖 |
| 740 | 1 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSe | y 72 | γQ |
| 720 2194 | 01 GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 7 | y 70 b 213 | Db Qy |
| 700 2134 | TheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal | ν | Db Qy |
| 680 2074 | l GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer | 20 6 | Db Qy |
| 660 2014 | 1 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn | 19 | Db Qy |
| 640 1954 | TATGILESerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet - | 18 | 4d 6y |
| 620 1894 | 1 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal | 18 6 | da Qy |
| 600 1834 | 1. ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys | . 17 | Qy Db |
| 580 1774 | 1. GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn | 17 | de Vo |
| 560 1714 | 1 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu | , 16 | 5 4d |
| 540 1654 | 21 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis |) 15 | dd VQ |
| 520 1594 | 01 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | Qy 5 Db 15 | п о |
| 500 1534 | 81 LysargGluIleValGlyValValGluProValProHisaspGluThrTyrCysaspPro | Qy 4 Db 14 | п о |
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| 420 1294 | 01 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | Qy 4 Db 12 | |
| 1234 | | Db 11 | п |

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           AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA
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                                                                                                                                                                                                                                                                ATTGAGGAACAGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC
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Acton, S. Laurene. and Robison, K. Earl
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LASWNYNTNITEENVQMMNAGDKWSARIKEQSTLAQMYPLQEIQNLTVKLQLQALQQ
NGSSVLSEDKSKRLNTILNTMSTIYSTGKYCNDNDQECLLLEPGINETNANSLDYNE
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RNGANEGFHEAVGEINSISAATPKHLKSIGLLSPDFQEDNETELNGALTYGFTL
RNGANEGFHEAVGEINSISAATPKHLKSIGLLSPDFQEDNETELNGALTYGTL
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DYSFIRYTTRTLYQFQPQBALCQAAKHEGPLHKCDISNSTEAGGYLFUMLRLGKSSPW
TLALEMVGAKMNWRPLLNYEEPLFTWIKKDOKNKSFVGWSTDWSPYADQSIKVRISL
KSALGDKAYEWNDNEMYLFRSSVAYAMAQYFLKVKNQMILFGEEDVRVANLK PRISFN
FFYTAPKNVSSIIPRTEVEKAIRWSRSRINDAFRLNDNSLEFIGIQPPVQPVS
FFYTAPKNVSSIIPRTEVEKAIRWSRSRINDAFRLNDNSLEFIGIQPTCGPPNQPPVS
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LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
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| human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 | AX431513 396 bp DNA linear PAT 28-JUN-2002 N Sequence 1 from Patent WO0239997. AX431513 AX431513.1 GI:21656345 | ValGlnThrSerPhe 805 | TyralaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800 | IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780 | IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760 | SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740 | GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720 | PheasnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700 | GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680 | TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660 | ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640 | AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620 | ValargProLeuLeuAsnTyrPheGluProLeuPheThTTrpLeuLysAspGlnAsnLys 600 | GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560 | TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540 |

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                                                AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla
                                                                                                       TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA
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US-09-978-385-2 (1-805) x AF241254 (1-3405)
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Best Local Similarity:
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                                                                                                                                                                     TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
                                                                     ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCCGAAGACCTGTTC
                                                                                                  IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turner, A.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functional expression as a captopril-insensitive carboxypeptidase J. Biol. Chem. 275 (43), 33238-33243 (2000)
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RIGANBGFHEAVGEIMSLSAATPKHLKSIGLLSDEFGEDNETELFLIKQALTIVGTL
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DYSFIRYYTRTLYQFQFOEALCQAAKHBGPLHKCDISNSTEAGQKLFNMLRLGKSEPW
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KSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMLFGEEDVRVALMLKPRISEN
EFVTAPKNVSDILPRTEVEKAIMSRSSINDAFRLNDNSLEFLGIQPTLGPPNQPPVS
INLIVEGVVMGVIVVGIVILLFTGIRDRKKKNKARRGENPYASIDISKGENNPGFQNT
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laswavntntteenvomnnacdkwsaflkeostlaowyploeiqnitykloloaloo
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rlwaneswrseygkoliplyeeylvlknemaranhyedygdxwrgdyeyngvocydxs
rgqliedvehtfeeikplyehlhayvraklmnaypsyispigclpahlligdmwgrfwt
nlysljypfgokpnidytdaaydoawldaorifkeaekefvsvolipnmyogfwensmlt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="angiotensin converting enzyme-like protein"
/protein_id="AAF78220.1"
/db_xref="GI:8650466"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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| Db 1 | P 49 | B & | | | . • | g b | 04 B 7 | ov Db | рь Оу | VQ E | γ Q | Db QQ | D | Db Db | Qy | 5 S | Ъ. | 0v 0b | , Q | DЪ | Qy | Дb |
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| 441 LySGLIALALAUThrILeVALGLYThrLeuProPheThr 411 | 421 IleGlyLeuLeuSerProAspPheGlnGluAspAsno | 401 H1SG1IALAVALG1yG1UT1eMetSerLeuSerAlaAla | 381 TyraspMetAlaTyralaAlaGlnProPheLeuLeuAr | 1184 TGCACAAAGGTGACAATGG | 1124 AAAGCACTCTGCCACACATTGGGACCTGGGGC | 1064 CCTAATATGACTCAAGGATTCTGGGAAAATT | 11011 PROPERTY OF THE PROPERTY | 944 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATG | 884 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAG 281 LeuThrValProPheGlyGlnLysProAsnTleAsnVa | 02% CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTI 261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGl | 24 | 221 GinLeuIleGluAspValGluHisThrPheGluGlu | 704 GATTATTGGAGAGGAGACTATGA | 644 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAG | 181 GluGluTyrValValLeuLysAsnGluMetalaa. | л L | 524 TGCTTATTACTTGAACCAGGTTTGAATGAATAATAGTGG | 464 AATACAATGAGCACCATCTACAGTACTGGAAAAGTT | 12 | | 101 GlnGlnAsnGlySerSerValLeuSerGluAspLvs | Db 344 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAG |
| TyrMetLeuGluLysTrpArg 460 TACATGTTAGAGAAGTGGAGG 1483 | SluThrGluIleAsnPheLeuLeu 440 | ThrProLysHisLeuLysSer 420 | '9AsnGlyAlaAsnGluGlyPhe 400 | SHISGluMetGlyHiSIleGln 380 | GlyAspPl GGCGACTT | WINTASPProGlyAsnValGln 340 | hePhev CTTT | TACTGATGC/ | HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | TTCCTATATCAGTCCAATTGGA 8 JPheTrpThrAsnLeuTvrser 2 | oSerTyrileSerProileGly 26 | <pre>LleLysProLeuTyrGluH1sLeu 240 </pre> | PGlyTyrAspTyrSerArgGly 220 | ≥-8 | AAGCAGCTGAGGCCATTATAT 64 | lyLysGlnLeuArgProLeuTyr 180 | LaAsnSerLeuAspTyrAsnGlu 160 | TAACCCAGATAATCC | sAsnProAspAsnProGlnGlu 14 | AGCAAACGGTTGAACACAATTCTA 463 | ickasciicasciscasscicii 40 erlysardienascubrileie 10 | TCAAGCTTCAGCTTGCAGCCTTCTT AC |

| | ValGlnThrSerPhe 805 | 801 2504 | Qy Db |
|----------------------|---|-------------|------------|
| 800 2503 | TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp | 781 2444 | Дb |
| 780 2443 | LePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro | 88 6 | DB 45 |
| 760 2383 | CETTPLEUILEVALPhedlyValValMetGlyValITLeValValGlyILeValITLeLeu | 4 (3 (| D |
| 740 2323 | GCCTAGAGTTTCTC | . 60 1 |) B 4 |
| 720 2263 | LysalaileArgMetSerArgSerArgIleJ | | D 42 |
| 700 2203 | "Weasn2nePneValTnrAlaProLysAsnVa. | a -4 c | 2 8 2 |
| 680 2143 | LIMETILELEUPHEGLYG | | B & |
| 660 2083 | TyrLeuPheArgSerSerVal | 4 0 1 | Db Qy |
| 640 2023 | ArgileSerLeu | י ס ג | DB 02 |
| 620 1963 | AsnSerPheValGlyTrpSer | ōō | Db 49 |
| 1903 | alargProLeuLeuAsnTy. TAAGGCCACTGCTCAACTAC | 4 (| B 8 |
| 1843 | GlyLysSerGluProTrpThrLeual | 8 8 | 2 D |
| 1783 | LysCysAspIleSe | 4 4 | da Ao |
| 540 1723 | <pre>1. TyrGlnbheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis </pre> | 0 1 | ₽ <i>Q</i> |
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| 500 | ysargGluIle AGCGAGAGATA | 15 4 | da Qy |
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REFERENCE
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No..
                              1 MetSerSerSerSrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
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Submitted (25-JUL-2000) Takami Komatsu, the Institute of Medical Science, Virology; 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:komatsu@ims.u-tokyo.ac.jp, Tel:81-3-5449-5283(ex.75283),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning, expression analysis and chromosomal localization of a novel ACE like enzyme % \left( 1\right) =\left\{ 1\right\} 
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NLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNNTQGFWENSMLT
DPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLL
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/product="ACE2
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/dev_stage="adult"
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/clone="kaia4505"
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FFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEELGIQPTLGPPNQPPVS
IWLIVFGLVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFQNT
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                                                          GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTTCCGTCTGAATGACAAC
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Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Clone from S. Wiemann, Email s.wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
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Homo sapiens mRNA; cDNA DKFZp434A014 (from clone DKFZp434A014);
partial cds.
AL110224
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp434A014) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at http://www.mips.biochem.mpg.de/proj/cDNA/
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Mammalia; Eutheria; Primates;
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| pol pol BASE COU ORIGIN | polyA_signal 32663271 polyA_site 3281 COUNT 1058 a 630 c 740 g 913 t IN | |
| Alignmen Pred. No Score: Percent Best Loc Query Ma DB: | <pre>pment Scores: 1. No.: 2.</pre> | |
| us-09-97 | 8-385-2 (1-805) x HSM800880 (1-3341) | |
| Qy Db | 2 SerSerSerTrpLeuLeuLeuSerLeuValalaValThrAlaalaGlnSerThTIle 21 | |
| Qy 2 Db 6 | 2 GluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPheTyr 41 | |
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| Qy 10 Db 30 | 2 GlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsn 121 | |
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| Qy 20 Db 60 | 21 TyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGln 221 | |
| Qy 22 Db 66 | 22 LeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeuHis 241 | |
| Qy 24 Db 72 | 2 AlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCys 261 | |
| Qy 26 Db 78 | 22 LeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeu 281 | |

| ln 661 | 642 LeinbheargSerserValalaTvralaMetArgGlnTvrPheLeuLvsValLvsAsnG | 0ν |
|-----------------------------|--|----------|
| C 1 | 63 ATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG | Db |
| yr 641 | 2 IleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMe | Qy |
| rg 621 .GG 1862 | 02 SerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysValA | ду рь |
| sn 6 - AT 1 | 82 ArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysA | Qy Db |
| al 581 TA 1742 | 62 LysserGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnV | Оу |
| ly 561 GA 1682 | 42 CysaspileSerāsnSerThrGluālaGlyGlnLysLeuPheāsnMetLeuārgLeuG | Фр |
| 16 | 22 GlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis | Qy Db |
| Yr 5: | 502 SerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeuTy | Оу |
| la 501 CA 1502 | 82 ArgGluTleValGlyValValGluProValProHisAspGluThrTyrCysAspProA | Qy Db |
| s 48 † G 14 | 462 MetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMetLy | Qу Дъ |
| rp 461 { GG 1382 | 42 GlnalaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArgT | Qy Db |
| Lys 441 AAA 1322 | 22 GlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluTleAsnPheLeuLeu | Qу |
| TT 1262 | 402 GlualaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSerII | Qу Db |
| is 401 AT 1202 | 382 ASPMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPheHi: | Фу |
| yr 381 AT 1142 | 362 ThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGlnTyr | Qy Db |
| ys 361 GC 1082 | 342 AlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCy | Ф |
| ys 341 | nMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGlnI | ОУ |
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| la 301 CC 902 | 82 ThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGlnAl | Qу |

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1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCACTGGGATCAGAGATCGGAAGAAGAAAATAAAGCAAGAAGTGGAGAAAATCCTTAT 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnProTyr 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTTGGCATTGTCATCCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPhe 681
                                                                                                                                                                                                                                                                                              Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
                                                                                                                                                                                                                                                                   Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Sequence 71 from Patent WO0140466.
AX463938
                                                                                                                                                                                                                                      Genentech
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                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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| ln 380 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGl | 361 | Qy |
|--------------------------|--|------|-------|
| <u> </u> | | 1060 | Db |
| t 360 | ysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuM | 341 | Ωу |
| | CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTC | | Db |
| ت د د | roAsnMetThrGlnGlvPheTrpGluAsnSerMetLeuThrAsnProGlvAsnValG | 321 | Qγ |
| | AGTTCTTTGTATCTGTTGGTC | 940 | Db |
| | laTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyL | 301 | Qy |
| II AG 939 | TGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACC | 880 | Дb |
| ln 300 | uThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspG | 281 | Qy |
| FT 879 | GCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGGTAGATTTTGGACAAATCTGTACT | 820 | Db |
| er 280 | ProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrS | 261 | Qy |
| GA 819 | CCTATGTGAGGGCAAAGTTGATGATGCCTATCCTTCCTATATCAGTCCAATTG | 760 | Db |
| Y 2 | lisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleG | 241 | Qy |
| TT 7 | | 700 | В |
| O. | lnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisL | 221 | Qy |
| GC 69 | GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCG | 640 | ДЬ |
| ly 2 | .spTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgG | 201 | Qy |
| GG 63 | GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATG | 580 | ДЬ |
| 1у 2 | luGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrG | 181 | Qy |
| 11 AT 57 | | | Db |
| yr 18 | rgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuT | 161 | Qy |
| | TGCTTATTACTTGAACCAGGTTTGAATGAATAATGG | 460 | Db |
| <u> </u> | CysLeuLeuCluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsn | 141 | Qy |
| AA 45 | AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCC | 400 | Db |
| į. | nThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGln | 121 | Qy |
| TA 39 | | 340 | DЬ |
| eu 1 | lnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIle | 101 | Qy |
| 3 - 3 | CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCA | 280 | Дb |
| Ō | GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAla | 81 | Qy |
| 111 3CC 279 | AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTAAAGGAACA | | Db |
| - | AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeu | 61 | Qy |
| AA 2 | TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATT | 160 | Дb |
| Ë | TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnVal | 41 | Qy |
| Phe 40 TC 159 | 1 11eG1uG1uG1nA1aLysThrPheIeuAspLysPheAsnH1sG1uA1aG1uAspLeuF | | Db QY |
| NCC 99 | | | Db |

| GACCAGAACAAGAATTCTTTTGTGG | AACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACC | 2198 | Дb |
|-------------------------------------|---|-------------|----------|
| SASPGINASDLYSASDSETPHEVALGLY 605 | 6 AsnTyrPheGluProLeuPheThrTrpLeuLysAspGlr | 586 | Qγ |
| -AAGAACATGAATGTAAGGCCACTGCTC 2197 | 9 TGGACCCTAGCATTGGAAAATGTTGTAGGAGC-AAGAAC | 2139 | 망 |
| | 6 TrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsr | 566 | Qy |
| :ATGCTGAGGCTTGGAAAATCAGAACCC 2138 | 9 AAGGCCCTGAACCCCCTTTTTTTGTGTAGCAATATGCTG | 2079 | ДЪ |
| | 6AsnMetLeu | 556 | Qy |
| AATATATGTACATCTGGAACCCCTCAA 2078 | 9 GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATAT# | 2019 | B |
| 555 | 5 | 555 | Qy |
| TTATCTGCCAGAAGCAAATTTAGCCAA 2018 | 9 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCI | 1959 | В |
| 555 | 5 | 555 | Qy |
| GGTAATTGGAAGGAAAGAGCGGTTTAG 1958 | 9 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAAT | 1899 | ДЬ |
| 555 | | 555 | Qy |
| ATACAACAATTGGGTGGGCCACCTCTT 1898 | 9 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAA | 1839 | ф |
| 555 | | 555 | Qy |
| TCAAAATGTCCTCATTTACAAACCAAA 1838 | ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAA | 1779 | рь |
| 555 | | 555 | Qy |
| TCATTTCCATGCCTAGGTTTGTATTTG 1778 | AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTT | 1719 | Вр |
| 555 | | 555 | Qy |
| CAGAAACTGTT-GTAAGAAATACCTCA 1718 | AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAA | 1660 | Db |
| GlnLysLeuPhe 555 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLys | 541 | Qy |
| GCAGCTAAACATGAAGGCCCTCTGCAC 1659 | TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCT | 1600 | 밁 |
| AlaAlaLysHisGluGlyProLeuHis 540 | TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAla | 521 | Qy |
| | | 1540 | Db : |
| PheIleArgTyrTyrThrArgThrLeu 520 | . AlaSerLeuPheHisValSerAsnAspTyrSerPheIle | 501 | Qγ |
| ProHisaspGluThrTyrCysaspPro 500 | . LysArgGluIleValGlyValValGluProValProHis | 481 1480 | Qу Db |
| AGTGGATGAAAAAGTGGTGGGAGATG 14 | TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGG | 1420 | В |
| InTrpMetLysLysTrpTrpGluMet 480 | TrpMetValPheLysGlyGluIleProLysAspGlnTrp | 46 | Qy |
| AGAGAAGTGGAG | AAACAAGCACTCACGATTGTTGGGACTCTGCC | 6 | Db |
| oPheThrTyrMetLeuGluLysTrpArg 460 | LysGlnAlaLeuThrIleValGlyThrLeuPr | 441 | Qy |
| AAACTTCCTG | ATTGGTCTTCTGTCACCCGATTTTCAAGAAGA | 0 | рь |
| snGluThrGluIleAsnPheLeuLeu 4 | ${\tt eGlyLeuLeuSerProAspPheGlnGluAspAsnG}$ | 4 | Qy |
| | CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGG | 4 | 망 . |
| laAlaThrProLysHisLeuLysSer 4 | isGluAlaValGlyGluIleMetSerLeuSerAlaAl | 40 | ν0 |
| | AA H | œ | 윰 . |
| euArgAsnGlyAlaAsnGluGlyPh | rAspMetAlaTyrAlaAlaGlnProPheLeuLeuAr | æ | Q V |
| SCTCATCATGAGATGGGGCATATCCAG 1179 | TC | 1120 | Db |

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           Mammalia; Eutheria; Primates; Caraniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 2262)

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RS Christopher_D.S. and Nicola,B.

MPROT15 polypeptide and MPROT15 polynucleotide
Patent: JP 199318472-A 2 24.NOV-1999;

SMITHKLINE BEECHAM (ORP PUBLIC LID CO
OS Homo sapiens (human)

PN JP 199318472-A/2

PD 24.NOV-1999

PF 22-JAN-1999 JP 1999014949

PF 22-JAN-1999 JP 1999014949

PF 13-MAY-1998 GB 9810373:2,18-AUG-1998 GB 9818009:4 PI
CHRISTOPHER D SAZAN, NICOLA BAGESU

PC C12N15/09, A61K31/00, A61
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MPROTI5 polypeptide and MPROTI5 polynucleotide.
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A61K39/395,A61K45/00,A61K48/00,C07K14/47,C12P21/02,C12Q1/68,
G01N33/15,
G01N33/50,G01N33/50,G01N33/566,G01N33/68//(C12P21/02,
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                                                                                     191 AlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn
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GlyValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPhe
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                                                                                                                                  AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly 130
                                                                                                                                                                                                                GCCTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACAAGAAATTCAGAAT 303
                                                                                                        GAGGTCGGCAAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAAAATGAGATG
                                                                               GCAAGAGCAAATCATTATGAGGACTATGGGGGATTATTGGAGAGGAGACTATGAAGTAAAT
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Location/Qualifiers
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
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| 1773 | GTCCATG | 1765 | В |
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| 590 1704 | GluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluPro 5 | 4 7 | Дy |
| 570 1644 | GlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeu 5 | <u>α</u> υ | Db Db |
| 550 1584 | GlnAlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAla : | NΩ | Ф |
| | erPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCys | | DP QV |
| 1476 | | 7 | Db |
| 510 | ${\tt ValProHisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyr:}\\$ | 491 | Qy |
| 490 1476 | AspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyValValGluPro (| 4 7 | Дb |
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| 430 1323 | roLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnglu | 411 1264 | ду В |
| 410 1263 | euLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeu | 391 1204 | рb |
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| 370 1143 | SThrLysValThrMetAspAspPheLeu CACAAAGGTGACAATGGACGACTTCCTG | 351 1084 | ОУ |
| 350 1083 | SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp | 331 1024 | Db Qy |
| 330 1023 | AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn | 311 964 | Фр |
| 310 963 | . IleaspValThraspAlametValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu | 291 904 | Qy Db |
| 290 903 | LeuThrValProPheGlyGlnLysProAsn TGACAGTTCCCTTTGGACAGAAACCAAAC | 271 844 | Дy |

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KEYWORDS
SOURCE
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ACCESSION
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Patent: WO 0070032-A 5 23-NOV-2000;
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Piddington, C.S., Petrie, C.R.,
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NLYPLTVPFAQKPNIDVTDAMMNOGWDAERIFOEAEKFTVSVGLHMTOGFWANSMLT
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                                                                                                                             HisalaTyrValargAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly
 Leu \verb|ThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln|
                                      TGCCTCCCTGCCCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACCCT
                                                                                                           CATGCCTATGTGAGGAGGAAGTTGATGGATACCTACCCTTCCTACATCAGCCCCACTGGA
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GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
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                                                     AGGATAAGCCTAAAATCAGCTCTTGGAGCTAATGCATATGAATGGACCAACAACGAAATG
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                                                                                                                             AATTCTTTTGTGGGGTGGAACACTGAATGGAGCCCATATGCCGACCAAAGCATTAAAGTG
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Clone distribution: MGC clone distribution information can be through the I.M.A.G.B. Consortium/ILINI at: http://image.llnl.gc Series: ITAK Plate: 31 Row: e Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

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COMMENT
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KEYWORDS
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             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., J
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G.,
                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Justitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Richards, S., Gibbs, R.A.
                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCTGTTCCGATCATCTGTTGCATATGCCATGAGAAAGTATTTTTCAATAATCAAAAAC
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                                                                  Mus musculus ACE2 mRNA for anic carboxypeptidase, complete cds
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Submitted (04-JAN-2001) Takami Komatsu, The insitute of medical science, Univesity of Tokyo, Laboratory of Genome Structure Analysis; 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan (E-mail:komatsueims.u-tokyo.ac.jp, Tel:81-3-5449-5283(ex.75283),
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Direct Submission
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Best Local Similarity: 89.45% 81.89% 83.01% 10 Mismatches: Conservative: Indels:

3.08e-290 3562.00

Matches:

1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20

21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40

247 ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAAGCTGAAGACCTGTCT

41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln TATCAAAGTTCACTTGCTTCGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA 366

| 7 ATTGGTCTTCTGCCATCCGATTTCAAGAAGATAGCGAAACAGAGATAAACTTCCTACTG 15 | DB 45 |
|---|-------|
| 21 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLe | OV |
| 87 CATGAAGCTGTTGGAGAAATCATGTCACTTTCTGCAGCTACCCCCAAGCATCTGAAATC | Db |
| 01 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysS | Qy |
| 27 TATGACATGGCATATGCCAGGCAACCTTTCCTGCTAAGAAACGGAGCCAATGAAGGGTT | рь |
| 81 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgA | Qy |
| 67 TGTACAAAGGTCACAATGGACAACTTCTTGACAGCCCATCACGAGATGGGACACATCC | DЪ |
| 61 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGl | Ω |
| TCTGGGACACGGAGACTTCAGAATCAAGAT | Db |
| ysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgTle | Qγ |
| 47 CCTCATATGACTCAAGGATTCTGGGCAAACTCTATGCTGACTGA | Db |
| roAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnVa | Qy |
| 87 GCTGGGATGCAGAAAGGATATTTC | ф |
| TrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLe | Qy |
| 27 TTGACTGTTCCCTTTGCACAGAAACCAAACATAGATGTTACTGATGCAATGAATG | Дb |
| 1 LeuThrValProPheGlyGlnLysProAsnIleAspValThrA | Ωу |
| 67 TGCCTCCCTGCCCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTA | 망 |
| 61 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyr | Qy |
| 07 CATGCCTATGTGAGGAGGAAGTTGATGATACCTACCCTTCCTACATCAGCCCCACTGG | Db |
| 41 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIl | Qу |
| 7 CAGTTGATGAAGATGTAGAACGTACCTTCGCAGAGATCAAGCCATTGTATGAGCATCT | DЬ |
| 21 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuT | Qy |
| 7 GATTATTGGAGAGGGACTATGAAGCAGAGGGAGCAGATGGCTACAACTATAACCG | ф |
| 01 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGl | Qy |
| 27 GAAGAGTATGTGGTCCTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGG | DЬ |
| 1 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrC | Qy |
| 667 AGGCTCTGGGCATGGGAGGGCTGGAGGGCTGGGCAAGCAGCTGAGGCCGTTGTAT 726 | В |
| 61 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTy | Qγ |
| | В |
| 41 CysLeuLeuCluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGl | Qy |
| 4 | Db |
| .21 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGl | Qy |
| 101 GlnGlnAsnGlySerSerValLeuserGluAspLysSerLysArgLeuAsnThrIleLeu 120 101 GlnGlnAsnGlySerSerValLeuserGluAspLysSerLysArgLeuAsnThrIleLeu 120 111111::: | Db Qy |
| 27 CAAAGTTTCTCACTACAAGAAATCCAGACTCCGATCATCAAGCGTCAACTACAGGCCII 40 | ф |
| 81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysL | Qy |
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441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460

| 800 pValGlnThrSerphe 805 | Qy |
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| 781 TyralaSer-IleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAs | Qу |
| | Db 2 |
| 761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro | Qy |
| ::: | Db 2 |
| 741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 407 ATATGGCTGATTATTTTTGGTGTTGTGATGGCACTGGTAGTGGTTGGCATCATCATCCTG | Qy Db 2 |
| 721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer | ОУ . |
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| 701 GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn | Qy |
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| 681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal | Qу (|
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| 661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer | Оу 6 |
| :: :::::: | Db 21 |
| 341 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn | Qy 6 |
| ::: | Db 21 |
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| | Db 20 |
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| | Db 19 |
| R1 ValargProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys | Qy 5 |
| | Db 19 |
| 61 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn | Qy 5 |
| | Db 18 |
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| | Db 16 |
| 81 LysargGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 5 | Qy 4 Db 16 |
| 61 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 4 | Qy 4 Db 15 |
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                                                                                               286 AAGATGAGTGAGGCTGCAGCCAAATGGTCTGCCTTTTATGAAGAACAGTCTAAGACTGCC
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                     81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
                                                                                                                                                AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
                                                                                                                                                                                                    TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCCAA
                                                                                                                                                                                                                                TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
                                                                                                                                                                                                                                                                                                         ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAGGCTGAAGACCTGTCT 225
                                                                                                                                                                                                                                                                                                                                                     IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe
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//Broteil_id="GL18993.1"
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                           441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg
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                                                                 TATGACTCGATGGACATTGGAAAAGGAGAAAGCAATGCAGGATTCCAAAACAGTGATGAT
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181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
                              481 MGNYTNTGGGCNTGGGARWSNTGGMGNWSNGARGTNGGNAARCARYTNMGNCCNYTNTAY 540
                                                                                                                                                                                                                                             101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
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                                                                                                                                                                                                                                                                                                                                                                     AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
                                                          ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
                                                                                          TGYYTNYTNYTNGARCCNGGNYTNAAYGARATHATGGCNAAYWSNYTNGAYTAYAAYGAR
                                                                                                                        CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
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Sequence 3 from Patent W00070032.
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zace2: a human metalloenzyme
patent: WO 0070032-A 3 23-NOV-2000;
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1 (bases 1 to 2415)
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1. .2415
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                                                                                                                                                                                    501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
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                                                                                                                                                                                                                                                                                                                                       TGGATGGTNTTYAARGGNGARATHCCNAARGAYCARTGGATGAARAARTGGTGGGARATG 1440
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                                                                                                                                                                                                                                                                       LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
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-DB=N_Geneseq_101002 -QPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LCCAL -OUTEMT=pto -NORM-ext +HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09978385_@CGN_1_1_396_@runat_28022003_104716_1332 -NCPU=6 -ICPU=3
-WARN_TIMEOUT=30 -THREADS-1 -XGAPOS=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
                      1: //SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980 DAT: *
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3: //SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982 DAT: *
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                                                                   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; human;
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                                                                                                                         Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing infertility. The present sequence represents a cDNA encoding the human zaces protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and entercolitis, as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a converting enzyme in the converting enzyme in the expression of a converting enzyme in the converting enzyme in the expression of a converting enzyme in the converting enzyme in the expression of a converting enzyme in the converting enzyme in t
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| TRECCATCCCAAGCTTGGGACTTGGGACGGCGACTTCAGGATCCTTATTTTTTTT | ThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValax | 221 GINLeuIleGLUASpValGLHISThrPheGLUGIUILELysProLeuTyrcluHisLeu 240 | 61 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGl | |
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| Qy 721 SerLeuGluPheLeuglyIleGlnProThrLeuglyProProAsnglnProProValSer | 1955 661 2015 681 2075 701 | | Qy 541 IYGINFREGIRFREGIRGIAKALENCYSGINAIAKALYSHISGIIGIYPFOCHUHIS | 1295 ATTGGTC 441 LYSG1n, 1315 AAACAAA 461 TrpMetv 11111111 1415 TGGATGG 481 LYSATGG 1111111 1475 AAGCGAG 501 AlaSerI 1535 GCATCTC |
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| 400 1234 | TyraspMetAlaTyralaalaGlnProPheLeuLeuArgasnGlyAlaasnGluGlyPhe | 381 1175 | P 64 |
| 380 1174 | CysThrLysValThrMetAspAspPheLeuThrAlaH1sH1sGluMetGlyHisIleGln | 361 1115 | pb Qy |
| 360 1114 | ysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeum | 4. (7) | Db Qy |
| | AsiMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsn | 9 N | Db Qy |
| 320 994 | laTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePI | 301 935 | dg VQ |
| 300 934 | rValProPheGlyGlnLysProAsnIleAspValI | 281 875 | DP OA |
| 280 874 | CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer | 261 815 | DP QA |
| 260 814 | HisalaTyrValargAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly | 241 755 | pb Qy |
| 240 754 | GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu | ס ט | ОУ |
| 220 694 | AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyr | 6 N | Дy |
| 200 634 | . GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly | (π ⊢ | P dd Vo |
| 180 574 | ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLy | 16 51 | d Vo |
| 160 514 | CysLeuLeuLeuGluProGlyLeuAsnGluIleMctAlaAsn | & ⊔ | Qy db |
| 140 454 | ASnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu | 35 | d da |
| 120 394 | GlnGlnAs CAGCAAAA | 10 33 | dd Vo |
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                                                           Local Similarity:
                                                                                                                                                                                                                                    The present sequence encodes a human angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The sequence of the full length ACE-2 cDNA was determined from a clone obtained from a cDNA library prepared from mRNA of a human heart of a subject who had congestive heart failure. ACE-2 has significant sequence homologies with ACE enzymes, and has also been shown to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure related diseases and conditions, such as hypertension, congestive heart failure, chronic heart failure, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding angiotensin converting enzyme-2 (AC polypeptide useful for detecting an ACE-2 therapeutic for treating hypertension, congestive heart failure, myocardial infarction,
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LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet
                                                                                                                                   CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer
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                                                                  CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG
                                                                                  ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln
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GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn
                                                 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
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                              PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal
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                       TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT
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             Claim 1;
                           screening
                                  Novel genes encoding angiotensin antisense or antigene agents for
                                                        P-PSDB;
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                                                                                                        11-DEC-1997;
                                                                                                                      11-DEC-1997;
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                                                                                           MILLENNIUM PHARM INC
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/note= "This region is referred

specifically claimed in claim 26

82...135
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/product= "Human angiotensin
(ACE-2)"
                                                                                                                                                                                                                                                  Location/Qualifiers 82..2499
                                                                                                                                                                                                                                                                                                                 converting
                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                        2496
             English
                                                                                                                                                                      "Human
                                                                                                                                                                                                                                                                                                                 enzyme-2 (ACE-2)
                                                                                                                                                                                                                                                                                                                                                            ВP
                                   converting enzyme-2 useful therapeutics, diagnostics a
                                                                                                                                                                        mature
                                                                                                                                                                        angiotensin
                                                                                                                                                                                                      , as
                                                                                                                                                                                                                                     converting
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                                                                                                                                                                                                                                                                                             peptidyl dipeptidase
eart failure; CHF;
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                                                                                                                                                                                                                                      enzyme-2
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No
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cDNA. ACE is also referred as peptidyl dipeptidase A. Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein levels for determining the disease or condition associated with an aberrant protein level.
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| Qy | Qу | Дy | g V | dg VQ | Db Qy | Db Qy | ОУ | Db 94 | g 94 | Db Qy | Db Qq | Qу | US-(| Alic Prec Scon Perc Best Quen DB: | 99999999999888 |
|--|--|--|--|--|---|--|--|---|--|--|--|--|--|---|--|
| 241 HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260 | 221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240 | 201 ASpTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220 | 181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200 | 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180 | 141 CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160 | 121 ASnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140 | 101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120 | 81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100 | 61 ASDMetASDASDA1aGlyASpLySTrpSerAlaPheLeuLySGluGlnSerThrLeuAla 80 | 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60 | 21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40 | 1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20 | 09-978-385-2 (1-805) x AAD02758 (1-3396) | gnment Scores: 0 Length: 3396 d. No.: 4291.00 Matches: 805 cent Similarity: 100.00% Conservative: 0 t Local Similarity: 100.00% Mismatches: 0 ry Match: 100.00% Indels: 0 Gaps: 0 | cDNA. ACE is also referred as peptidyl dipeptidase A. Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein levels for determining the disease or condition associated with an aberrant protein level. Sequence 3396 BP; 1034 A; 659 C; 772 G; 931 T; 0 other; |

| δõ | Db Qy | Qy Db | Qy Db | Qy Db | Qy Db | Qy | Qy dd | Qy dd | Db Qy | Qy Db | Qy db | Qy db | Оу | Qy Db | Qy Db | Qy dd | dd Db | Db |
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| 601 | 581 1822 | 561 1762 | 541 1702 | 521 1642 | 501 1582 | 481 1522 | 461 1462 | 441 1402 | 421 1342 | 401 1282 | 381 1222 | 361 1162 | 341 1102 | 321 1042 | 301 982 | 281 922 | 261 862 | 802 |
| AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 6 | ValArgProLeuLeuAsnTyrPheGluProLeuPheThTTrpLeuLysAspGlnAsnLys 6 | GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 5 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 5 | TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 5 | AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrargThrLeu 5 | LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 5 | TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 4 | LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 4 | IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 4 | HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisieuLysSer 4 | TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 4 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGin 3 | LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 3 | ProAssMetThrGlnGlyPheTrpGluAssSerMetLeuThrAspProGlyAssValGln 3 | AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 3 | LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 3 | CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 2 | |
| 20 | 00 881 | 80 821 | 60 761 | 40 701 | 20 641 | 00 581 | 80 521 | 60 461 | 40 401 | 20 341 | 00 281 | 80 221 | 60 161 | 40 101 | 20 041 | 81 | 80 | 61 |

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                                                                                                                                                                                                                                                                                                                                                                                     angiotensin converting enzyme-2; ACE-2; body weight disorder;
/rtag= a
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                                         Location/Qualifiers 82..2499
                       /*tag=
                                                                                                                                     gene; ss.
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   "Human angiotensin converting enzyme-2 (ACE-2)
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 US-09-978-385-2 (1-805) x ABK87623

(1-3396)

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The present invention describes a new method of treating a body weight compound. The invention can be used for treating body fat by compound. The invention can be used for treating body weight disorders, compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a state associated with lipid metabolism. The method is used for treating compound weight loss, rapid weight gain, anorexia, cachexia, bulimia, congestive heart failure, chronic heart failure, left ventricular typercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate, congestive heart failure, chronic heart failure, left ventricular typercholesterophy, acute heart failure, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease and Huntington's disease), myocardial infarction, cardiomyopathy, systemic inflammation response syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and composed composed composed injury, carebral vasospasm after subarachonid are tracker, reperfusion composed including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, condex of greater than 23 (preferably 24.9)kg/m^2. The present nucleic acid sequence encodes the human ACE-2 protein of the invention.
BB
                           Percent Similarity:
Best Local Similarity:
                                                                                                                       Query Match:
                                                             Score:
                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000;
29-MAY-2001;
                                                                                                                       Sequence 3396 BP; 1034 A; 659 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 383-387; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-2001;
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DB; AAU99701.
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; 2001US-0870382.
; 2001US-371741P.
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139..2496
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Solomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rder and increasing muscle mass converting enzyme-2 modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein"
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M, Stricker-Krongrad
                                                                                                                       772 G; 931 T; 0 other;
                             Length:
Matches:
Conservative:
Mismatches:
              Indels:
 0000
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compound
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| 400 1281 | TyraspmetalaTyralaalaGlnProPheLeuLeuArgAsnGlyAlaasnGluGlyPhe | 381 1222 | Db Oy |
|-------------|---|-------------|---------|
| 380 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln | 361 | Qу |
| 1221 | | 1162 | |
| 360 | LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet | 341 | dg |
| 1161 | | 1102 | VQ |
| 340 1101 | ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | 321 1042 | Оy |
| 320 | AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu | 301 | Qу |
| 1041 | | 982 | |
| 300 | GlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln | 281 | Оy |
| 981 | | 922 | |
| 280 921 | <pre>FrpThrAsnLeuTyrSer GGACAAATCTGTACTCT</pre> | 261 862 | Db 94 |
| 260 861 | HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly | 241 802 | Оy |
| 240 801 | GluHisThrPheGluGluIleLysProLeuTyrGluHisLeu | 2 4 | Фр |
| 220 741 | AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly | 201 682 | . pb Qy |
| 200 | GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly | 181 | рь |
| 681 | | 622 | 29 |
| 180 | uSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr | 161 | 9d |
| 621 | | 562 | V0 |
| 160 | euGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu | 141 | 9d 4d |
| 561 | | 502 | |
| 140 501 | ysValCysAsnProAspAsnProGlnGlu AGTTTGTAACCCAGATAATCCACAAGAA | 4 2 | Фр |
| 120 441 | ArgLeuAsnThrIleLeu GGTTGAACACAATTCTA | 101 382 | Db 04 |
| 100 | LeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu | 81 | Фр |
| 381 | | 322 | |
| 80 321 | GluGlnSerThrLeuAla SAACAGTCCACACTTGCC | 61 262 | рь |
| 60 | TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln | 41 | оу |
| 261 | | 202 | Оу |

| 761 IlePheThrGlyTleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780 | | |
|--|---------------|--|
| 2302 ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2361 | | |
| leTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLe | | |
| | b 22 | |
| erLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSe | | |
| 701 GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720 | | |
| 122 TTTAAFTTCTTTGTCACTGCACCTAAAAATGTGTCTGAFATCATTCCTAGAACTGAAGTT 21 | 21 | |
| 81 PheasnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 70 | ў б | |
| 661 GINMETILELEUPREGIYGIUGIUASPVALAIGVALAIASRILEULYSPTCATGIIESET 680 | | |
| 002 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT 20 | ъ 20 | |
| 641 TyrLeupheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660 | | |
| 621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640 | | |
| TTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGT | | |
| rPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIl | | |
| 581 VALAIGETOLEULEUASIIYIENEETUETOLEURINETIITIILEULYSASPAINASIILYS 000 | | |
| 62 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT 18 | . 17 | |
| 61 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 58 | | |
| 541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560 | | |
| 42 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 17 | | |
| 521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540 | | |
| | ъ ъ 15 | |
| .laSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLe | | |
| 481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500 | Oy 4 Db 15 | |
| .462 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGAT | | |
| rpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluM | | |
| 02 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTAC | b 14 | |
| 41 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 46 | У 4 | |
| | 13 | |
| 21 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluTleAsnPheLeuLeu 44 | Ž Ž | |
| 401 HisGluAlaValGlyGluIlleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420 | | |
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The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polynucleotides. ACE-2 is also known as peptidyl dipeptidase A (EE 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, a therosolerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility. The present sequence is human full-length ACE-2 cDNA. The ACE-2 gene is located on the x chromosome at p21-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polypeptide, known as angiotensin converting enzyme-2, useful for treating or preventing the development of an abnormal bloc pressure or related diseases, e.g. hypertension, heart failure or
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Mismatches:
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21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr CAGCAAAATGGGTCTTCAGTGCTGTCAGAAGACAAAGAGCAAACGGTTGAACACAATTCTA GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrI1eLeu GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 501 621 180 561 160 140 441 120 381 100 321 80 261 60 201 40 141

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                                                                                                                    gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                   PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -
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                                                                                 Sequence
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z
                                                                                   821 G; 1052 T; 0 other;
Length: Matches:
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                                                                  GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT
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             Human; novel human protein; NHP; ss; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary; neuroprotective; nootropic; antiparkinsonian; arti-human immunodeficiency virus; antiasthmatic; vasotropic; cardi hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsar antimanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction; gastrointestinal disorder; cardiovascular disorder; hypertension; pastrointestinal disorder; cardiovascular disorder; hypertension;
        coronary heart
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     arteriosclerosis;
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  anorexia;
obesity; bulimia;
                                                                                                                          anticonvulsant;
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CC rucleic acids that encode them and antibodies raised against them.
CC nucleic acids that encode them and antibodies raised against them.
CC rhe proteins, antibodies and nucleic acids are useful in the diagnosis,
CC prognosis, prevention and/or treatment or diseases and/or disorders
CC involving vasoconstriction, gastrointestinal disorders, cardiovascular
CC disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
CC coronary heart disease and arteriosclerosis), anorexia, obesity, bulinia,
CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC entral nervous system disorders, disorders of pulmonary system,
CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC panic disorder, learning disabilities, amyotropic lateral sclerosis,
CC psychoses, autism, sleep disorders), immune system disorders (e.g.
CC psychoses, autism, sleep disorders), immune system disorders,
CC central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC brain injury and/or stroke), infectious disease, diabetes mellitus,
CC brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC sepsis, acne, psoriasis and lupus erythematosus), neural system
CC sepsis, acne, psoriasis and lupus erythematosus), neural system
CC disorders, respiratory disorders, olfactory disorders and wound
CC disorders, respiratory disorders, and invention and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders -
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healing. The present sequence encodes an NHP is located on the X chromosomo
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/trans1_except= (pos:867..869,aa:Xaa)
/trans1_except= (pos:930..932,aa:Xaa)
/trans1_except= (pos:1707..1709,aa:Xaa)
/note= "Xaa= Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 GAACAGGCCAAGACATTTTTGGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCA
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                                                                       uProAlaHisLeuLeuGlyAspMctTrpGlyArgPhcTrpThrAsnLeuTyrScrLeuTh
                                                                                                                                  aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe
                                                                                                                                                                                                                                                                                                    uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTy 202
                                                                                                                                                                                                                                                                                                                                                             uTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGl 182
                                                                                                                                                                                                                                                                                                                                                                                                    uLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGl 102
                                                                                                               CTATGTGAGGCCAAAGTTGATGAATGCCTATCCTTATATCAGTCCAATTGGATGCCT
                                                                                                                                                                       GATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGC
                                                                                                                                                                                                                              TTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTT
                                                                                                                                                                                                                                             rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLe
                                                                                                                                                                                                                                                                                       GTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTA
                                                                                                                                                                                                                                                                                                                                              CTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGA
AGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGRCCTG
             CCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATYTGTACWSTTTGAC
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                                           tIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAs 682
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                                                                                                                                AAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT
                                                                                                                                                                         eSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLe
                                                                                                                                                                                                                     TTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACA 1354
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huntington's disease; schizophrenia; mania; dementia; paranoia; panic disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; immune system disorder; hashimoto's thyroiditis; musculo-skeletal system disorders; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorder; pulmonary system disorder; central nervous system disorder; bone disorder; parkinson's disease; neurodegenerative disease; Alzheimer's disease; parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory, antibacterial, antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction; gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; nootropic; antiparkinsonian; anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant; hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cachexia; male infertility; impotence; testicular cancer; lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimanic; immunosuppressive; cerebroprotective; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding novel human protein NHP #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC discarder learning disorders of pulmonary system (e.g. hypertension, erectile dysfunction, high blood pressure, coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia, CC cachexia, disorders of small intestine, disorders of reproductive system CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours candexia, disorders of pulmonary system, CC entral nervous system disorders, bone disorders, of pulmonary system, CC disease, Huntington's disease, Farkinson's CC disease, Huntington's disease, Farkinson's CC disease, autism, sleep disorders, barning disorders, pearnoia, paranoia, ceptionses, autism, sleep disorders), immune system disorders (e.g. psychoses, autism, sleep disorders), immune system disorders, central nervous system disorders (e.g. multiple sclerosis, isohaemic CC brain injury and/or stroke), infectious disease, diabetes mellitus, CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, CC sepsis, acne, psoriasis and lupus crythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human proteins (NHP) and the nucleic acids that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, prognosis, prevention and/or treatment or diseases and/or disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2911 BP; 896 A; 570 C; 655 G; 788 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 297-298; 318pp; English.
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                      102 nAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsnTh 122
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                                                                   GTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCA
                                                                                                               tTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGl 102
                                                                                                                                                              GAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAAT 274
                                                                                                                                                                                       tAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMe 82
                                                                                                                                                                                                                                                               AAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT 214
                                                                                                                                                                                                                                                                                      nSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMe 62
                                                                                                                                                                                                                                                                                                                                                           GAACAGGCCAAGACATTTTTGGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCA 154
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                                                                                                                                                                                                  GCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTT
                                                                                                                                                                                                                                                                             GGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACGACAGCCT 2192
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                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGAT
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                                   coding sequence #2.
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                 IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer 170
                                                 ATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGAAAGCTGGAGATCT
                                                                                             GACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCATCTACAGTACTGGA
                                                                                                         AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly
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This is coding sequence #2 of human MPROT15. The MPROT15 polynucleotide and polypeptide sequences can be used for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing of peptide
                                                                                                                                                                                                                                                MPROT15 polypeptide and MPROT15 polynucleotides - useful itreatment of hypertension, myocardial diseases, apoplexy, diseases, nervous denaturation, Alzheimer's disease etc.
                                                                                                                                                                                                     Claim 18; Page 15; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease; hormone; cytokine.
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| 550 | ${\tt GlnAlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAla}$ | 531 | Qy |
|------|--|----------------|---------|
| 1524 | TATTACACAAGGACCCTTTACCAATTCCAGTTTCAAGAAGCACTTTGT | 1477 | Ф |
| 530 | SerPheIleArgTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCys | 511 | Qy |
| 1476 | | 1476 | В |
| 510 | $\tt ValProHisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyr$ | 491 | Qy |
| 1476 | GACCAGTGGATGAAAAGTGGTGGGAGATGAAA | 1444 | DЬ |
| 490 | AspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyValValGluPro | 471 | Qy |
| 1443 | CCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCCAAA | 1384 | В |
| 470 | ProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGluIleProLys | 451 | Qy |
| 1383 | GACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTG | 1324 | В |
| 450 | AspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeu | 431 | Qy |
| 1323 | TCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTCTGTCACCCGATTTTCAAGAA | 1264 | ДЪ |
| 430 | SerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnGlu | 411 | Qy |
| 1263 | CTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGAAATCATGTCACTT | 1204 | Db |
| 410 | LeuLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeu | 391 | Qγ |
| 1203 | ACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTT | 1144 | Dр |
| 390 | ThralaHisHisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAlaGlnProPhe | 371 | δõ |
| 1143 | CTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAATGGACGACTTCCTG | 1084 | рь |
| 370 | LeuGlyLysGlyAspPheArgIleLeuMetCysThrLysValThrMetAspAspPheLeu | 351 | Qy |
| 1083 | TCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCCCACAGCTTGGGAC | 1024 | DЪ |
| 350 | SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp | 331 | Qy |
| 1023 | GCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGGATTCTGGGAAAAT | 964 | 망 |
| 330 | AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn | 311 | Qγ |
| 963 | ATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAG | 904 | 망 |
| 310 | IleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu | 291 | Qy |
| 903 | | 844 | 망 |
| 290 | TrpGlvArqPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn | 271 | Q V |
| 843 | | 784 | B |
| 270 | AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet | 251 | νQ |
| 783 | GAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAAT | 724 | 뭥 |
| 250 | GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn | 231 | Ϋ́ |
| 723 | GGGTAGATGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAACATACCTTT | 664 | Db |
| ũ | lyValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPh | | Qγ |
| 663 | | | В |
| 210 | .laargAlaasnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAs | 91 | γQ |
| E03 | GALDYALGY_LySGIDLeuArgProLeuTyrGLUGLUTyrValYaLLeuLySASGGLUMET | 171 · 544 · | g Qy |
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antiarthritic;

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                                             zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc metallopeptidase; blood pressure; zinc metallopeptidase; blood pressure; zinc protease; heart failure; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         converting enzyme is a zinc metallopeptidase that plays roles in blood C pressure regulation and fertility. Zace2 can be expressed by standard CC recombinant methodology. Zace2 polypeptides are useful for treating an CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis). CC diseases associated with inflammation like arthritis and enterocolitis. CC as targets for identifying modulators of zinc protease activity, for CC screening or identifying new angiotensin-converting enzyme (ACE) CC inhibitors, and as a basis for rational drug design for inhibitory CC molecules. The nucleic acids can be used to detect the expression of a Cace2 gene in a biological sample, as probes for in vivo diagnosis and CC for detecting and localizing Zace2 gene expression in tissue samples, CC to determine whether a subject's chromosomes contain a mutation in the Cace2 gene, and to detect aberrations associated with the Zace2 locus. CC conditions, including left ventricular systolic dysfunction, progressive crenal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing cancer. Such constain a conditions associated with the cace2 and the mouse cancer to the conditions and treatment of atherosclerosis. Zace2 agonists may be considered to treat infertility while Zace2 antagonists are used for inducing confertility. The present sequence represents a cDNA encoding the mouse cace?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 104-109; 125pp; English.
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27-AUG-1999;
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                                   41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA
                                                                                             IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe
                                                                                                                                                MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr
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                                                                          ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAAGCTGAAGACCTGTCT
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/note= "the coding"
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CATGAAGCTGTTGGAGAAATCATGTCACTTTCTGCAGCTACCCCCAAGCATCTGAAATCC
              HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer
                                                                            TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe
                                                                                                                                           CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln
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                                                                                                                                                                                        AAAGTTGTCTGCCACCCCACAGCTTGGGATCTGGGACACGGAGACTTCAGAATCAAGATG
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TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp
                                                           ATTGTCACTGGGATCAAAGGTCGAAAGAAGAAAAAATGAAACAAAAAGAGAAGAGAACCCCT
                                                                                              ATATGGCTGATTATTTTTGGTGTTGTGATGGCACTGGTAGTGGTTGGCATCATCCTG
                                                                                                                                                                                                                                            IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu
                                                                                                                                                                                                                                                                                                        AGCCTGGAGTTTCTGGGGATTCACCCAACACTTGAGCCACCTTACCAGCCTCCTGTCACC
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Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -

Disclosure; Page 113-118; 125pp; English.

as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressiv renal impairment, scleroderma renal crisis, congestive heart failure du to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis, infertility. The present sequence represents a cDNA encoding invention relates to the metalloenzyme Zace2. protein Zace2, an angiotensin the progressive mouse

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molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atheroscle-crosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing infertility. The present seminora "arrenant".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for
                                                                                                                                                                                                                                                                                                                                                                                                                      screening or identifying new angiotensin converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of
                                                               infertility. The page encoding the human
                                                               The present sequence represents a degenerate sequence human zace2 protein.
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Sequence 2415 BP; 494 A; 218 C; 398 G. 335 Η, 970 other;

US-09-978-385-2 (1-805) x AAC84367 (1-2415)

Query Match:

Best Local Similarity:

Percent Similarity:

0 3509.00 80.00% 80.00% 81.78%

Length:
Matches:
Conservative:
Mismatches:

Indels: Gaps:

Alignment

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  AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly
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                                            GARGARTAYGTNGTNYTNAARAAYGARATGGCNMGNGCNAAYCAYTAYGARGAYTAYGGN
                                                                                        GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
                                                                                                                             MGNYTNTGGGCNTGGGARWSNTGGMGNWSNGARGTNGGNAARCARYTNMGNCCNYTNTAY
                                                                                                                                                                     {\tt ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr}
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                                                                                                                                                                                                                                                                                                    <u>AAYACNATGWSNACNATHTAYWSNACNGGNAARGTNTGYAAYCCNGAYAAYCCNCARGAR</u>
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                                                                                                                                                                  TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
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                                                                          Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
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Qy Qy Db

20 99 Best Local Similarity: Query Match: DB:

Percent Similarity:

7.79e-294 3119.00 85.94% 83.43% 72.69%

Length:
Matches:
Conservative:

3474 730 22 51 72 10

No

US-09-978-385-2

 $(1-805) \times AAS42515$

(1-3474)

Mismatches: Indels: Gaps:

39

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Alignment Scores:
                                                     The invention relates to novel human molecules for disease detection and treatment (mddt proteins) and the polynucleotides encoding them. The MDDT polynucleotides and polypeptides are useful for diagnostic and therapeutic purposes e.g. to diagnose and treat cell proliferative disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g. adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g. acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and many more diseases given in the specification. The present sequence encodes an mddt protein of the invention.
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Wright RJ,
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16-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                    New disease detection and treatment molecule polynucleotides and polypeptides, useful for diagnosis and treatment of arteriosclerosis, cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus, asthma and multiple sclerosis
                                                                                                                                                                                                                                                                                                                                               WPI;
                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; antidiabetic; antiasthmatic; neuroprotective; osteopathic; antiarthritic; cell proliferative disorder; arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma; leukaemia; breast cancer; autoimmune disorder; AIDS; acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.
                                                                                                                                                                                                                        Claim 1; Page 139-140; 183pp; English.
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J, Yap PE, Yu
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E, Flores V, Fong WT,
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2000US-0205232.
2000US-0205285.
2000US-0205286.
2000US-0205287.
2000US-0205323.
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, Dahl CR, Dam TC, Daniels SE;
WT, Greenawalt LB, Hillman JL,
en BH, Russo FD, Stockdreher TK,
Bradley DL, Bratcher SR, Chen V
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, Daffo A;
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| yHisIleGlnTyrAspMetAlaTyrAlaAlaGlnPro-PheLeuLeuArg-AsnGlyAla 396 | 377 yı | Qy |
|--|-------------------------------|----------|
| TCCTTATGTGCACAAAGGGTAACAATGGACGACTTCCTGACAGCTCATCATGAGATGGG 1 | ⊅ . | ДЬ |
| IleLeuMetCysThrLys-ValThrMetAspAspPheLeuThrAlaHisHisGluMetGl | 358 I | Qy |
| ValGlnLysAlaValCysHis-ProThrAlaTrpAspLeuGlyLysGlyAspPheArg- 35 ::: | H-5 | Qy |
| yLeuProAsnMetThrGlnGlyPheTrp-GluAsnSerMetLeu-ThrAspProGlyAs 3 | 6 – u | Qу |
| GlnAlaTrpAspAlaGlnArgIlePheLysGluAla-GluLysPhePheValSerValG 31 | о—в | Qу |
| SerLeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAs 29 | 0-8 | Db Qy |
| lyCysLeuProAlaHisLeuLeuGlyAspMetTrp-GlyArgPheTrpThrAsnLeuTy 27 | n – n | Qy Db |
| euHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIle 2 | 0-1 | Qy Db |
| GlnLeuIleGluAspValGluHisThr-PheGluGluIleLysProLeuTyr-Glu | 0-4 | Qу |
| gGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerAy AGGAGACTATGAAGTAAATGGGGTAAATAGTGGATATGATTACAGCCC | | Qy . |
| uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAsp-Tyr-Gl | ~ | ОУ |
| pAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrG | | Db Qy |
| uLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgL | H - 0 | B 8 |
| ThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu | | D Qy |
| GluAspLysSerLys-ArgLeuAsnThrIleLeuAsnThrMet 12 ::: | | Db Qy |
| InAlaLeuGlnGlnAsnGlySerSerVa 10 | | Дy |
| nSerThrLeuAlaGln-MetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLe 95 | $\mathfrak{Q} = \mathfrak{Q}$ | Qy Db |
| IGIn-AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGlu | H — D | Qy |
| heTyrGlnSerSer-LeuAlaSer-TrpAsnTyrAsnThrAsnIleThrGluGluAsnV 5 ::: | 7 - P | Qу Db |

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RESULT 16
AAC84369
ID AAC84
XX AC84
XX AC84
XX AC84
XX Zace2
KW Zace2
KW Zace2
KW Zace2
KW Scler
KW Scler
KW AC84
XX A
             The invention relates to the metalloenzyme Zace2, an angiotensin-Converting enzyme is a zinc metalloeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an Converting the processed section of the converting and continuous bowel disease (e.g. Crohn's disease and ulcerative colitis). Conserved a stargets for identifying modulators of zinc protease activity, for Considered with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for Conserved and Conserved as a basis for rational drug design for inhibitory concludes. The nucleic acids can be used to detect the expression of a Conserved gene in a biological sample, as probes for in vivo diagnosis and Conserved gene in a biological sample, as probes for in tissue samples, to detecting and localizing Zace2 gene expression in tissue samples, concerning whether a subject's chromosomes contain a mutation in the Cace2 gene, and to detect abstractions associated with the Zace2 locus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 112-113; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse; antiarthritic; bradykinin inactivator; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piddington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, e.g. Crohn's disease and ulceratiated with inflammation such as arthritis
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          of ACE
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for treating hypertension of
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2415 BP; 488 A; 228 C; 397 G; 324 T; 978 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat_infertility while Zace2 antagonists are used for inducing
       721
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                                  HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly
                                                                                        GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
                                                                                                                                                      GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
CAYGCNTAYGTNMGNMGNAARYTNATGGAYACNTAYCCNWSNTAYATHWSNCCNACNGGN
                                                                    CARYTNATHGARGAYGTNGARMGNACNTTYGCNGARATHAARCCNYTNTAYGARCAYYTN
                                                                                                                                    GAYTAYTGGMGNGGNGAYTAYGARGCNGARGGNGCNGAYGGNTAYAAYTAYAAYMGNAAY
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ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
                                                                                                                                                                        GTNAARCCNYTNYTNAAYTAYTTYCARCCNYTNTTYGAYTGGYTNAARGARCARAAYMGN
                                                                                                                                                                                                                                                                                      GGNAAYWSNGARCCNTGGACNAARGCNYTNGARAAYGTNGTNGGNGCNMGNAAYATGGAY 1740
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 WPI; 1991-036748/05
                         Soubrier F,
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                                                                                                                                                                                                                                                                                                                                                          10-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                           AAQ10328 standard; DNA; 2477
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                                                                         05-JUL-1989;
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                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                         human testicular angiotensin conversion enzyme; tACE;
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                                                                                                                                                                                                                                                                                              sterility;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2477 BP; 536 A; 811 C; 695 G; 435 T; 0 other;
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                               TrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLeu 222
                                                                                                                                                                                                                     CAGCTCGAGCCAGATCTGACGAATGTGATGGCCACATCCCGGAAATATGAAGACCTGTTA
                                                                                                                                                                                                                                                      LeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLeu
                                                                                                     TyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyr 202
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   TGGAGGTCTATGTACGAGACACCATCCCTGGAG---
                                                                       TACGTGGAACTCATCAACCAGGCTGCCCGGCTCAATGGCTATGTAGATGCAGGGGACTCG
                                                                                                                                               TGGGCATGGGAGGGCTGGCGAGACAAGGCGGGGAGAGCCATCCTCCAGTTTTACCCGAAA
                                                                                                                                                                                  TrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGlu
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                                                                                                                                                                                                                                                                                                                            MetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysLeu 142
                                                                                                                                                                                                                                                                                                                                                                       CTAGAACGGGCAGCGTGCCTGCCCAGGAGCTGGAGGAGTACAACAAGATCCTGTTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGATGTGAACCAGTTGCAGAACACCACTATCAAGCGGATCATAAAGAAGGTTCAGGAC
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1826 GGCTTCAGTAGGCCGTGGCCGGAAGCCATGCAGCTGATCACGGGCCCAGCCCAACATGAGC
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                     561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
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                                                                                                                                                                    TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis
                                                                                                   LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu
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                                                                          AAGTGTGACATCTACCAGTCCAAGGAGGCCGGGCAGCGCCTGGCGACCGCCATGAAGCTG
                                                                                                                                                                                                                        GGGGCCAAGTTCCACATTCCTTCTAGCGTGCCTTACATCAGGTACTTTGTCAGCTTCATC
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                                                                                                                                                                                                                                                                                                                                  Lys \texttt{ArgGluTleValGlyValValGluProValProHisAspGluThrTyrCysAspPro}
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                                                                                                                                                                                                                                                                                                                                         receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-admenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                        Fragments of the genes comprising a polymorphic site may be used als primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 114-115; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphic pattern comprising polymorphic encoding specific proteins, with reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human angiotensin-converting enzyme (ACE) coding region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotides 1451-1783 in intron 16.
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GluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAla
                                                                                                                                                                                                                                  ValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGlu 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt PheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsnLeupheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsnLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeupheLeup
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SerThrAspTrpSerProTyrAlaAspGlnSer
                                                                CCGCTGCTGGACTGGCTCCGCACGGAGAACGAGCTGCATGGGGAGAAGCTGGGCTGGCCG
                                                                                                                          ProLeuPheThrTrpLeuLysAspGlnAsnLys-----AsnSerPheValGlyTrp---
                                                                                                                                                                                                                                                                                                                                                                              AlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAla
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                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                       Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                              DNA of
                                                                                                                                                                                                                                                                                        27-JUN-2002
                                                                                                                                                                                                                                                                                                   AAK99395
                                                                                                                                                                                                                                                                                                             AAK99395 standard; DNA;
                                                                                                                                                                                                                                                                                                                                3689 CAGTACAACTGGACGCCGAACTCCGCTCGCTCA
                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                             APP related human homologue hCP51674.
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                     Location/Qualifiers
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04-APR-2002 WO200226820-A2. /note= "No start codon" /product= "Protein of human homologue hCP51674" /*tag= g

148..3945

01-OCT-2001; 2001WO-EP11345

14-JUN-2001; 29-SEP-2000; 2000US-236893P 2001US-298309P

SAON) NOVARTIS AG. NOVARTIS-ERFINDUNGEN VERW GES MBH

Cohen D, Dengler UJ, Reinhardt MWHM, Zusm Zusman Finelli AL, Freuler F, Konsolaki

2002-315796/35

New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease -

Example 4; Page 93-94; 129pp; English.

The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-specific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonucleotide, double stranded RNA molecule ribozuma or particularly as actions. stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynucleotide sequence represents the DNA of the APP related human homologue hCP51674.

Sequence 4022 BP; 856 A; 1262 C; 1174 G; 728 Τ, 2 other;

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Query Match:
DB:
                 Percent Similarity:
Best Local Similarity:
                                          No ::
                                                  Scores:
7.74e-120
1337.00
61.05%
41.73%
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LeuGlyLysGly---AspPheArgIleLeuMetCysThrLysValThrMetAspAspPhe
                                                                                   SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp
                                                                                                                                      GCTGATGATTTCTTCACCTCCCTGGGGGCTGCTGCCGTGCCTCCTGAGTTCTGGAACAAG
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                                                       TCGATGCTGGAGAAGCCAACCGACGGGCGGGAGGTGGTCTGCCACGCCTCGGCCTGGGAC
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                                                                                                                                                                                                                  (first entry)
 /*tag= :
23..3944
                                 Location/Qualifiers 23..51
                                                                                                                                             converting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes pre-ACE. In the mature protein the 29 amino acid signal peptide is absent. ACE hydrolyses angiotensin I and/or kinins, most notably bradykinin. Vectors contg. the given sequence are used to produce ACE for therapeutic use eg to hydrolyse kinins implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4024 BP;
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                                             MetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu
                                                                                                              ValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrIleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeu 39
                              ATGGCCACATCCCGGAAATATGAAGACCTGTTATGGGCATGGGAGGGCTGGCGAGACAAG
                                                                                    GTGTGCCACCCGAATGGC-----AGCTGCCTGCAGCTCGAGCCAGATCTGACGAATGTG
                                                                                                                                            GAGCTGGAGGAGTACAACAAGATCCTGTTGGATATGGAAACCACCTACAGCGTGGCCACT
                                                                                                                                                                    LysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGlyLys 131
                                                                                                                                                                                                  ThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGluAsp 111
                                                                                                                                                                                                                                                          -----CTGAAGTACGGCACCCAGGCCAGGAAGTTTGATGTGAACCAGTTGCAGAACACC 2167
                                                                                                                                                                                                                                                                                                                                                                          TGGAACGAGTATGCCGAGGCCAACTGGAACTACAACACCAACATCACCACAGAGACCAGC
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                                                                                                                                                                                                                                                ### ATCCCCTTCAGCTACCTCGTCGATCAGTGGCGCTGGAGGGTATTTGATGGAGCATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCCTTACATCAGGTACTTTGTCAGCTTCATCATCCAGTTCCAGGTTCCACGAGGCACTG
                                                                                                                                                                                 AAGGAGAACTATAACCAGGAGTGGTGGAGCCTCAGGCTGAAGTACCAGGGCCTCTGCCCC
                                                                                                                                                                                                                                                                     LeuProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGluIlePro
                                                                                                                                                                                                                                                                                                                                   GluAspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThr
                                                                                                                                                                                                                                                                                                                                                                                  CTCTCAGTGTCTACGCCCAAGCACCTGCACAGTCTCAACCTGCTGAGCAGTGAGGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGln
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                                                                                TyrSerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeu
                                                                                                                 CCAGTGCCCAGGACTCAAGGTGACTTTGACCCAGGGGCCAAGTTCCACATTCCTTCTAGC
                                                                                                                                                                                                                LysaspGlnTrpMetLysLysTrpTrpGluMetLysargGluIleValGlyValValGlu
                                                                                                                                                                                                                                                                                                                  AGCGAC - - - GAGCATGACATCAACTTTCTGATGAAGATGGCCCTTGACAAGATCGCCTTT
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Command line parameters:

WODEL-frame+_p2n.model -DEV-xlp
-O-cgn2_1/USPTO_spool/US09978385/runat_28022003_104716_1351/app_query.fasta_1.967
-DB-EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -HIR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINIEN=7000000000
-USER-US09978385_@CGN_1_1_2874_@runat_28022003_104716_1351 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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   Xgapop 10.0,
Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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4291
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em_gss_inv: *
em_gss_pln: *
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gb_est3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | a a | α | } | Result No. |
|---|---|--|---|----------------|
| 444 441 443 | 335 | 22254 | 1 1 2 3 3 3 4 4 4 4 7 7 7 7 7 11 11 11 11 11 11 11 11 11 11 | WO. |
| 544 543 543 543 542 541 539 538 | 588.5 588.5 575.5 564.5 564.5 5849 | 643 625 622 615 | 4249 1445 11054.5 1048.5 1048.5 1048.5 1023 1023 1023 901 864 857 749.5 687 687 684 680 672.5 659.5 669.5 | Score |
| 12.66 | 13.8 13.7 13.5 13.4 13.2 12.9 12.8 | | 33.8 33.8 33.8 224.6 224 | Query Match |
| 432 965 965 775 628 418 | 666 725 751 471 606 728 728 | 492 348 773 887 347 | | Length |
| 10 13 13 13 13 13 10 | 13 13 13 13 10 10 10 10 | 10 9 13 13 | 111 11 1 | DB |
| AW258 BI825 BI453 BI103 BI103 BM187 BM290 BM290 BB687 AW026 | BI686319 BI821905 BI8289673 AW358360 BI914635 AW322773 AW322773 AW026259 BE138336 AB138336 | W2602 03973 18309 11967 W8485 | AKC032938 AL551235 AKC008530 AL913504 BG401683 BG962298 BIF561069 BG7722079 BF789159 AA162058 BH652968 BH652968 BG428060 BM030353 BH660866 BM460886 BG428060 BM0130353 BG772384 BI852537 BI831019 BI831019 BI784147 | ID |
| 58861 um74f04 58861 um74f04 25221 6030719 23308 6031701 03238 602889701 03238 50288701 87251 pgm2n.p 90186 EST5767 87602 BB68760 26258 wv10g07 | .6319 60331 1905 60303 8973 60307 88360 42453 4635 60317 2773 uc52b 6259 wv1052b 6253 ug51d | 0204 un74f(0204 un74f(738 DKFZp4(0308(0308(0275(0373) 60275(0373) 1L3-C1 | BC03293 BC03293 BC40168 BC40168 BC40168 BC40168 BC50168 BC50168 BC5029 BC782135 BC782135 BC42806 BC428 | Description |

ALIGNMENTS

| REFERENCE AUTHORS TITLE | ORGANISM | KEYWORDS | VERSION | ACCESSION | | DEFINITION | Locus | RESULT 1 BC032938 |
|--|--------------|----------|------------------------|-----------|----------------------------------|------------|--|----------------------|
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3337) Strausberg,R. Direct Submission | Homo sapiens | HTC. | BC032938.1 GI:21432080 | BC032938 | A) 2, clone IMAGE:4830668, mRNA. | erting enz | BC032938 3337 bp mrNA linear HTC 17-JUN-2002 | |

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Ilssue Procurement: Miklos Palkovits, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 34 Row: 1 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11225608
This clone has the following problem: frame shifted.

Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anup Madan,
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Stephanie Rodrigues, Amy Sanchez and Michelle
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                                                               TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet
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             LysargGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro
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                                                                                                                                                                  ValGlnThrSerPhe 805
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                                          Prime, mRNA sequence
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                     668 GluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAla 687
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                                                                                                                                                       CTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="placenta" 6; Site_1: NotI; Ist strand cDNA /Note="Vector: pcMvSPoRT 6; Site_1: NotI; Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpoRT 6
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                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Yanaka,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer denome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-Oka,K., Wang,K.H., Weitz,C., Whittaker,C., Willining,L., Toyo-Oka,K., Wang,K.H., Weitz,C., Whittaker,C., Willining,L., Weitz,Charles, W., Wang,K.H., Weitz,C., Wang,K.H., Weitz
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M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Wagner, L., Barsh, G., Blake, J., Boffelli, D., Boinga, N., Barsh, G., Blake, J., Boffelli, D., Boinga, N., Barsh, G., Blake, J., Boffelli, D., Boinga, N., Bortina, T., Barsh, G., Blake, J., Boffelli, D., Boinga, N., Boin
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/db_xref="MGD:MGI:1902242"
/db_xref="taxon:10090"
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/db_xref="GI:12842767"
/db_xref="MGD:MGI:1917258"
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/translation="MLSLGNSEPWTKALENVYGARNMDVKPLLNYFOPLEDWILKEQNR
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/translation="MLSLGNSEPWTKALENVYGARNMDVKPLLNYFOPLEDWILKEQNR
/KNGTVPFLEEDVYDALVYGGIIILIVTGIKGRKKKNET
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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/note="putative"
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                                                                                                                                                                                                                                                                                                      CTGGAGTTTCTGGGGATTCACCCAACACTTGAGCCACCTTACCAGCCTCCTGTCACCATA
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                               80 aGlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLe 100
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CCAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCT
                                                                                                                                                                nAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAl 80
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Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5243048"
/clone_lib="NIH_MGC_121"
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                                                                                                                                                                                                                                                                                                                                                                                  Email: ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_WC_75"
/clone_lib="NIH_WC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: sfiI (ggcgctgggcc); Site_2: SfiI (ggcgattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGGCGGCGACATG-dT(30)BN-3' (where B = A' C, Or G and N = A, C, G, Or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                                                                                                                                                                        /clone="IMAGE:4594140"
                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548 ThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThr
663 GGCATATTGCTATTACGGAGTACTTTTTAAAGTAAACATCG-----ATGATCTTTGGGG
                                                                                                         610 T---GGAGATAAGCA-TATGACTGGACG---ACATGAATTGTCCTGTNCCGATCATCTGT
                                                                                                                                                                627 aLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerVa
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ThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyr 515
                                                    AAGTGGTGGGAGATGAAGCGGGAGATCGTTGGTGGTGGAGCCTCTGCCTCATGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov d column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="NGI_CGAP_CO24"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: galf; Cloned unidirectionally. Primer: Oligo d'Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NGI_CGAP Library."
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and
                                                                                                              /clone="IMAGE:5296531"
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                                                                                          /lab_host="DH10B"
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BG722079.1 GI:14001266
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1 (bases 1 to 635)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11752 row: j column: 05
High quality sequence stop: 606.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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603255121F1 NIH_MGC_97 Homo sapiens
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/db_xref="taxon:9606"
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                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                        Plate: LLAM9811 row: i column: 09
High quality sequence stop: 676.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BF789159
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/clone="IMAGE:4223312"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH1OB (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPOI
                                                                      /db_xref="taxon:10090"
                                                                                                                             1. .965
                                                                                          /strain="FVB/N"
                                                                                                         /organism="Mus musculus"
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                                                                                                                               uHisAlaTyrValArg 245
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AA162058 55 bp mRNA linear EST 12-FEB-199 ms31h11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:608613 5' similar to SW:ACE_MOUSE P09470
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213 c 253 g 212 t 1 others
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                     186 LeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGly
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CTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGGGGATTATTGGAGAGGG
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, SOMATIC ;, mRNA sequence aa162058
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Arakawa,T., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                 ,Y. and Hayashizaki,Y.
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                                                                                      Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
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                                                                                                                                                                                                                                                                                                 212 AAGATGAGTGAGGCTGCAGCCAAATGGTCTGCCTTTTATGAAGAACAGTCTAAGACTGCC
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                                                                                                    ATGTCCAGCTCCTGGCTCCTTCTCAGCCTTGTTGCTGTTACTACTGCTCAGTCCCTC
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCCCCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage="adult"
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/clone="C630041D11"
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/strain="C57BL/6J"
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NHT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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602501471F1 NIH_MGC_75 Homo
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Plate: LLCM1367 row:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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/db_xref="ntacm:5066"
/clone="IMAGE:4615121"
/clone="IMAGE:4615121"
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/lab_host="DHIOB (TI phage-resistant)"
/lab_host="DHIOB (TI phage-resistant)
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                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
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/organism="Bos taurus"
/db_xref="taxon:9913"
                                                           Location/Qualifiers
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RESULT 15
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1 (bases 1 to 741)
                                                       Homo sapiens
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                                                                                                                                  mRNA sequence.
BG772384
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602722306F1 NIH_MGC_97 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
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138 roGlnGluCysLeuLeuGluProGlyLeuAsnGlu-IleMetAlaAsnSerLeuAsp 157
                                   418 TTCTCAAATACACATGAGCACCATCTACAGTACTGGAACCAGTCTGTAACCCCAGATAATC
                                                                                                         358 TCAGCACACACTGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAACACGGTTGAACACAA
                                                                                                                                          100 uGlnGlnAsn---GlySerSerValLeuSerGluAspLysSerLys-ArgLeuAsnThrI 119
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                                                        leLeu-AsnThr-MetSerThrIleTyrSerThrGly-LysValCysAsnProAspAsnP 138
                                                                                                                                                                               CAATATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCT
                                                                                                                                                                                                                                                                                                                                              TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
                                                                                                                                                                                                                                                                                                                                                                                                ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC
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                                                                                                                                                                                                                                                       AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTATAACGGAACAGTCCACACTTGCC
                                                                                                                                                                                                                                                                                                                             TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11417 row: j column: 20
High quality sequence stop: 797.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length clones and clones and clones and clones and cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Invitrogen). Research Genetics tracking code 013. this is a NIH_MGC Library."
244 c 230 g 157 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5167987"
/clone_lib="NIH_MGC_119"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCCCCAGTGCCC 799
                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Aaron Hsueh
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                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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725 ATCACCAAGGAGAACTATAACCAGGAGTGGTGGAGCCTCAGGCTGAAAGTACCAGGGCCT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM4500886 1154 bp mRNA linear EST AGENCOURT_6419622 NCI_CGAP_Ov44 Mus musculus cDNA clone IMAGE:5504231 5', mRNA sequence.
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity:
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                                                                                                                                                                                                                                        768 ArgLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAspIleSer
                                                                                                                                                                                                                                                                                                                                  748 ValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIleArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
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                                                                                                                                                                                                                                                                                            GTTGTGATGGCACTGGTAGTGGTTGGCATCATCCTGATTGTCACTGGGATCAAAGGT 441
                                                                                                                                                                                                                                                                                                                                                                                                  GlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleValPheGly
                                                                                                                                   LysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPhe 805
                                                                                                                                                                                                               CGAAAGAAGAAAATGAAACAAAAAGAGAAGAGAACCCTTATGACTCGATGGACATTGGA 501
                                                                                                                                                                                                                                                                                                                                                                              CACCCAACACTTGAGCCACCTTACCAGCCTCCTGTCACCATATGGCTGATTATTTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuGlyIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGGCCGCATCAATGATGTCTTTGGCCTGAATGATAACAGCCTGGAGTTTCTGGGGATT
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BI415293 900 bp mRNA linear EST 14-AUG-2001 602987289F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5143199 5', mRNA sequence.
BI415293
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High quality sequence stop: 756.
Location/Qualifiers
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/clone="IMAGB:5504231"
/clone="IMAGB:5504231"
/clone=Lib="NCI_CGAP_Ov44"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: ovary, PMSG-treated; Vector:
pCMV-SPOT6.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Library constructed by Life Technologies. Note:
this is a NCI_CGAP Library."
232 c 266 g 334 t 2 others
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                                              GluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSerIle
                              GAAGCTATTGGAG--ATAATGGCTCTCTCAGTGTCTACCCCCAAGCATCTATACAGTCTC
                                                                                         TTCATGCAGTACAAAGACTTACCCGTGACTTTCCGGGAGGGTGCCAACCCTGGTTTTCAT
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Plate: LLAM11353 row: a column: 24
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High quality sequence stop: 873.
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Tissue Procurement: Gilbert Smith,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Plate: LLAM12766 row:
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Tissue Procurement: Life Technologies,
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BM560537
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               /db_xref="taxon:9606"
/clone="IMAGE:5744856"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
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                                                                           Similarity:
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:5172423"
/clone_ib="NHH_MGC_119"
/tissue_type="medulia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for each of the control of the 
                                                                                                                                                                                                                                                                                        full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."
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Search completed: March Job time : 2390 secs 7, 2003, 09:47:36

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
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-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -MINMATCH+0.1 -LOOPCL=0
-MODEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIGT=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
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-USER=US99978385_GCGN_11_61_erunat_28022003_104717_1368 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-09-050-159-130
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| Sequence 1, Appli Sequence 45, Appl Sequence 45, Appl Sequence 45, Appl Sequence 15, Appli Sequence 1, Appli Sequence 1, Appli Sequence 108, Appli Sequence 4, Appli Sequence 202, Appli Sequence 256, Appli Sequence 16, Appli Sequence 17, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli | e 16 e 16 e 18 e 11 |

ALIGNMENTS

RESULT 1

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US-08-989-299-3
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                              TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3:
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                                                               REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E., Beth
              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keith
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LENGTH:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                     AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrXspTyrSerArgGly 220
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                                                                                                                                          GATTATTGGAGAGGAGTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 660
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| 1920 | GATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAAT | 1861 | Db |
| 0 | IleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAsp | 621 | Qy |
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| 580 | GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn | 561 | Qy |
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| 1680 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu | 541 1621 | Ф |
| 4 0 | TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHiSGluGlyProLeuHiS | 521 | Qу |
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| 5 N | AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | 501 | Qy |
| | | 1501 | Db |
| 500 | LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro | 481 | Qу |
| 1500 | | 1441 | |
| 480 | TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | 461 | Qу |
| 1440 | | 1381 | |
| | LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 441 | Qу |
| | | 1321 | Дъ |
| 440 | IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 | Qy |
| 1320 | | 1261 | Db |
| 420 1260 | HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | 401 1201 | Qy |
| 200 | TC Te | 381 1141 | Оу |
| 380 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 3 | 361 | Qу |
| 1140 | | 1081 | |
| 1080 | LysalavalCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 3 | 341 1021 | Qy Db |
| 340 | ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 3 | 321 | Qу |
| L020 | | 961 | |
| 960 | AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 3 | 301 | Qу |
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RESULT 2
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                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AIROLD E., Beth
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEPHONE: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                          TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HO
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          LENGTH: 3396 base pairs TYPE: nucleic acid STRANDEDNESS: single
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ZIP: 02109-2170
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                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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Best Local Similarity:
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                                           AGGATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG
                                                                                                                                                          GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG
                                                                                                                                                                                                                 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT
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                                                        ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet
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Query Match:
QΥ
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                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 40
LENGTH: 2350
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION:
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                                                                                                                    MetSerSerSerTrpLeuLeuLeuSerLeuValAlaVal-ThrAlaAlaGlnSerTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer
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                                                rIleGluGluGlnAlaLysThr-PheLeuAspLysPheAsnHisGlu-AlaGluAspLeu
                                                                                                 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAGACTGCTGCTCAGTCCAC
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PheTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThr-AsnIleThrGluGluAsnVa
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92.62%
92.37%
76.70%
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Matches:
Conservative:
Mismatches:
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| leMetSerLeuSerA 412 | 3/2 IAHLSHISGIUMETGlyHISIleGlnTyrASpMetAlaTyrAlaAlaGlnProPheLeuL 392 | D3 LYSGLYASP-PheArgile- | 85 AACGGACCCAGC | 314 PREPREVALSERVALGIYLE | 405 GATGCCAATGGTGGAC | 465 ACAAATCTGTACTCTTTGACE | 3/ SerProlledlyCysLeuProAlaHisLeu- | 85 TATGAACATCTTCAT | 37 Tyrgluhisia-entisalsmynisiuhisthr-pheglu | | 76 LOLEGIY FG. LIGIUTY FVAIVALLEGILYSASGGLUME LALA. 65 CATTATATGAAGAGTATGTGGTCTTGAAAAATGAGATGGCA. 98 SDTVTGLVAGGTVTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | | 58 VTAGGELLAGGE TAGGELLAGGE TAGGELAGGE TAGGELAGGELAGGE TAGGELAGGE TAGGELAGGELAGGELAGGELAGGELAGGELAGGELAGGE | | The Control of the Server of | | AAAACATGAATAATGCTGGGGACAAAATGGTCGTGCCTTTT | TCTATCAAAGTTCACTTGCTTCTTGGAATTATAACACCCAATATTACTGAAGAGAATGT 2 GlnAsnMetAsnAsnAlaGlyAsp-LysTrpSer-alaphacactcticCl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.Cl.C |

| RESULT US-08- ; Sequ | ਜੋ ਵ | g b | OV Db | Db Dy | Db | Db . | Ov Db | Ωу | Db | Db z | OV Db x | O4 D5 1 | Ov Db | Db Db | Oy Oy | Дy | Db Qy | Оу |
|---|--|-----------------------------|--|----------|----|------|-------|----|----|--|--|---------------------------------|-----------------------------------|-------|----------|----|----------|---|
| T 4 -481-626-1 uence 1, Application US/08481626 | 85 TTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 36 | 45 TCAGGATGTCCCGGAGCCGTATCA | 05 TGGTCACTGCCCCTAAAAATGTGTCTGATATCATT | | | | | | | 7 ThrLeuAlaLeuGluAsnVallus 11.00 11.00 12.00 1 | Carabeucys California Cal | 45 TGATTACTCCATTCGATATTACACAACA | 05 AACCTTGTGCCCCCATGATGAAACATACTG | | | | | AAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGGAAATCATGTCACTTTCTG 10 |

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                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2478 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CORVOL, Pierre TITLE OF INVENTION: Nuclei TITLE OF INVENTION: Testic TITLE OF INVENTION: Uses, TITLE OF INVENTION: Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,183
APPLICATION 04-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FR 89-09062 FILING DATE: 05-JUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-MAR-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                               No : :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finneg
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                209 ACATCAGCCCAGAGCCCAAACCTGGTGACTGATGAGGCTGAGGCCCAGCAAGTTTGTGGAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,
                                                                                                269 GAATATGACCGGACATCCCAGGTGGTGTGGAACGAGTATGCCGAGGCCAACTGGAACTAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                               15 ThralaalaGlnSer------ThrIleGluGluGlnAlaLysThrPheLeuAsp 30
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                                                               31 LyspheAsnHisGluAlaGluAspLeuPheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
   63
AsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMet 82
                                  AACACCAACATCACCACAGAGACCAGCAAGATTCTGCTGCAGAAGAACATGCAAATAGCC 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alhenc-Gelas, Francois
Hubert, Christine
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Uses, Especially for the In Vitro Screening for this
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               421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
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US-09-050-159-130

Sequence 130, Application US/09050159A

Patent No. 6197505

GENERAL INFORMATION:

APPLICANT: No. 6197505berg, Leif T

APPLICANT: Andersson, Maria K

APPLICANT: Linstrom, Per H

TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATILE OF INVENTION: COMPOSITIONS FOR USE THEREOF

CURRENT APPLICATION NUMBER: US/09/050,159A

CURRENT FILING DATE: 1998-03-27

CURRENT FILING DATE: 1998-03-27

CURRENT FILING DATE: 1998-03-27
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                                                        Query Match:
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Best Local Similarity:
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SEQ ID NO 130
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                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                             OTHER INFORMATION: Angiotensin I converting
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                                                                                                                                           SEQ ID NO 18
                                                                                                                                                                      APPLICANT: Phillips, M. Ian
APPLICANT: Mchuczy, Dagmara
APPLICANT: Mchuczy, Dagmara
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED '
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF
TILE REFERENCE: UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:0
-09-162-484-18
                       TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Phillips, M. Ian
APPLICANT: Mohuczy, Dagmara
APPLICANT: Mohuczy, Dagmara
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO
TITLE OF INVENTION: ANCIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF USE
FILE REFERENCE: UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/U
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EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3942
TYPE: DNA
ORGANISM: Rattus norvegicus
                                            2632 GATGGTCCCATTCCTGCCCACCTGCTAGGGAACATGTGGGCACAGACTTGGTCCAACATC
                                                                                                                            2572 CTGCATGCCTATGTGCGCCGCCTCCCTGCACCGCCATTATGGGTCTGAGTACATCAACCTG
                                                                                                                                                                                                               2524 -----CAAGACCTGGAAAAACTATACCAGGAGCTGCAGCCGCTCTACCTGAAC
                                                                                                                                                                                                                                                                                                               2482
                                                                                                                                                                                                                                                                                                                                                                                    2422 TTCCCAAAGTACGTGGACTTCTCCAACAAGATCGCCAAGCTCAACGGCTACTCTGATGCA 2481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1948 ACTGATGAAGCCAAGGCTAACAGGTTCGTGGAGGAGTATGACCGGACAGCCAAGGTGTTG
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279 TyrSerLeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetVal 298
                                                                                                                                                                                                                                                                  220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GlnAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 PheTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 ThrIleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeu 39
                                                                     LeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSer---TyrIleSerPro 258
                                                                                                                                                                                                                                                     GlyGlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHis 239
                                                                                                                                                                                                                                                                                                                                         GlyAspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArg 219
                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyr 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTGCTTTGGGTGTGGAAGAGCTGGCCAAGACAAGGTGGGGAAGAGCCATCCTTTCCCTTT 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTGTCTGTCACTGGAGCCTGATCTGACAAATATAATGGCCACGTCCCGGAAATACGAA 2361
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                                                                                                                                                                                                                                                                                                    GGGGATTCCTGGAGATCCTCATATGAGTCCGATGACTTGGAG-------
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                 US-09-440-325A-2
Sequence 2, Application US/09440325A
Patent No. 6280994
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                538 ProLeuHisLysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMet 557
                                                                                                                                                                       598 GlnAsnLys-----AsnSerPheValGlyTrp---SerThrAspTrpSerPro 612
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                                                                                                                                                                                                                                                                                                                                                                CCCCTGTACAAGTGTGATATCTACCAATCCAAGGAAGCAGGGAAGCTGCTGGCAGATGCC 3528
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Sheppard, Paul O.
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US-09-978-385-2 (1-805) x US-09-440-325A-2 (1-2082)
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LENGTH: 2082
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CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 3
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LOCATION: (1)...(2082)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                182 GluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHis---TyrGluAspTyrGly 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsn 121
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241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyr---ProSerTyrIleSerProIle 259
                                                                                                                                                                                                                              201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
                                                                                                                                                                                                                                                                                             625 CAYTAYGTNGARYTNWSNAAYAARGCNGCNCARYTNAAYGGNGTNNNNAARGAYATGGGN 684
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                                                                                                               GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGlu 181
                                                                                                                                                                              GCNYTNTGGCAYWSNAARTAYGARWSNGAYACNYTNGAR-----
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                                                            -CARGAYYTNGARMGNYTNTTYCARGARYTNMGNCCNYTNTAYYTNAAYCCN 774
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1774 YTNACNGGNGARWSNGARGTNWSNACNAAYGTNTTYATGACNTAYTTYAARCCNYTNYTN 1833
                                                                                                               1720 -----ytnytngcnytnaarytnggnwsnwaarccntggccngargtnytnaaratg 1773
                                                                                                                                                                                                       1660 WSNGGNCAYATGGGNCCNYTNCAYCARTGYGAYATHTAYAAYWSNAARATHGCNGGNAAR 1719
                                                                573 ValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeuPhe 592
                                                                                                                                                                                                                                                                                            1600 MGNMGNTAYTTYYTNWSNYTNGTNYTNCARTTYCARTTYCAYGARACNYTNTGYAARGCN 1659
                                                                                                                                                                                                                                                                                                                                                                                  1540 WSNGARGARTTYGAYCCNGGNGCNAARTTYCAYTTYWSNGCNGGNGTNCCNTAYATH 1599
                                                                                                                                                       553 LysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGluAsn 572
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                                                                                                                                                                                                                                             533 AlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAlaGlyGln 552
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                                                                                                                                                                                                                                                                                                                       514 ---ArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCysGlnAla 532
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                                                                                                                                                                                                                                                                                                                                                                                                                             494 AspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIle 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 LysLysTrpTrpGlu---MetLysArgGluIleValGlyValValGluProValProHis 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 ValGly-----LeuProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAsp 335
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08664596B Patent No. 5807703
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LENGTH: 467 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                    302 TATCAAAGTTCACTTGCNTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCA
                                                                                                        242 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 301
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                182 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 498-8224
60 nAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAl 80
                                                      41 TyrGlnSerSerLeuAla-SerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValG1 60
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MEDIUM TYPE: Floppy disk
                                                                                                                            21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETED PROTE
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                 1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Cambridge
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(617) 876-5851
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LaVallie, Edward
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Indels:
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US-08-905-223-27
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Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste
                                                                    US-09-978-385-2 (1-805) x US-08-905-223-27 (1-848)
                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                           Query Match:
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TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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MEDIUM TYPE: Floppy Disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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No.:
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                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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CITY: San Diego
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                                 612 ProTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLys 631
                                                                                                                                                                                                                                                                         LOCATION: 32.73
LOCATION 32.73
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7
OTHER INFORMATION: SEG LWLLFFLVTAIHA/EL
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
DEVELOPMENTAL STAGE: F
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                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: kidney
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide
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92101-3505
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501 West Broadway
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Duelert, Aymeric
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CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
                                       ; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27
   Alignment Scores:
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                                                                                                                                                                                        SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-10-04
                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/099,273
                                                                                                                                                                                                            SOFTWARE: Patent.pm
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 182
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                                                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                       TYPE: DNA
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                                                                                                                   FEATURE:
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                                                                                                                                                                      LENGTH: 848
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08157171 Patent No. 5736323
                                                                                                                                     APPLICANT: Soubrier, Florent APPLICANT: Hubert, Christine APPLICANT: COTVOL, Pierre TITLE OF INVENTION: Agents and TITLE OF INVENTION: the Geneti.
TITLE OF INVENTION: Enzyme NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street,
         COMPUTER READABLE FORM:
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                                                             CITY: Minneapolis STATE: MN
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08392625 Patent No. 5837485
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                     APPLICANT:
                APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
                                                                                                                                     APPLICANT: APPLICANT:
CORRESPONDENCE ADDRESS:
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No.:
                                                                                    APPLICANT:
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LENGTH: 192 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                              153 CACATCAACCTGGAGGGGCCCATTCCTGCTCACCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                              255 TyrileSerProileGlyCysLeuProAlaHisLeuLeu :::||||::: ||| :::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 LeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyr---ProSer 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIleLysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hillson, Randall A. REGISTRATION NUMBER: 31,838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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Wie, Thomas
                                                                                                                                 Rosenstein, Ralf
Kaletta, Cortina
Klein, Cora
                                                                               Kupke, Thomas
Jung, G nther
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Engelke, Germar
                                                                                                                                                                                                                      Schnell, No.
                                                                                                                                                                                                                                      G tz, Friedrich
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8700 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,625
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION ADTA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0652.0980002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                         2817 AACGACGTTAAAAATTTAGAAAAG---AATAATACAGTTTCTAAAATCAATGCG------ 2867
                                                                                                                                                                                                                           2754 GCATTTTTAAAAGAAAAG-----
                                                                                                                                                                                                                                                                                                                2742 TCTAATAACATT----------
                                                                                                                                                                                                                                                                                                                                                                                                     2682 AAGCAATTGCTCTCAGATATAAATGGATTTGGCTATCCCAAAAAAGACAGTTATAGTTTT 2741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2622 ATTAGGAATTATCACGAATTTTTTATGGATAAATATGGATTTGAACAACTAGTAAATTTA 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2562 ATTAGTGAAGCAGCATATATTCTCTGGTTATTATCTCCTAATCATTTTGGTACAAAAACT 2621
                                                                                   111 AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Мо
::
131 LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu 150
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STREET: 1100 New York Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 20005
                                                                                                                                                                                                                                                  71 AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn 90
|||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu------ 35
                                                                                                                                                                            91 LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu 110
                                                                                                                                                                                                                                                                                                                                                         51 AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AlaGluAspLeu-----PheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
                                                                                                                                   -----TATTTGCTTGCAATTCAAAATAACAGCCATATTGAAAATAACAGAA 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
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127.00
32.58%
18.14%
2.96%
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Conservative:
Mismatches:
Indels:
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| 3818 | | | Db , |
|------|---|--------|------|
| 437 | 0SerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIle | 42 | Οy |
| 3773 | | 371 | Db |
| 419 | 0HeuSerAlaAlaThrProLys | 41 | Qy |
| 3713 | ::::::: | 365 | Db |
| 409 | 8 GluGlyPheHisGluAlaValGlyGluIleMetSe | 39 | Qy |
| 3653 | 4 ATACTAAAAAAAGAACTAAAAAAAACATGGTAGGATTCGAATATTA | 359 | Дb |
| 397 | 7 | 38 | Qy |
| 3593 | 34 ATTATTGCTTTTGGAGATAATCGATTGCTATTAAATTTATTAAATGACAAGCATCTCATT | 353 | ДĎ |
| 386 | 4 | 38 | Qy |
| 3533 | AATTGGTTAAATAGGTTCGCAACTATTAGAGAAAAATGGCATATTCCAAAAGATGT | 3477 | Db |
| 383 | 4 | 36 | Qy |
| 3476 | : | 342 | Db |
| 363 | sGlyAspPheArgIleLeuMe | 34 | Qy |
| 3425 |)6 ACTGAAGAAGGCATTGACTCATTACCTTTTTGTCCAAGAATTATTTAT | 336 | Db |
| 343 | 38 AsnValGlnLysAlaVal | 3 3 | Qy |
| 3365 | GAATTATACAAATTTTTAAGAGAAATTTCATTTGAAAA | 3306 | 망 |
| 337 | 7PheTrpGluAsnSerMetLeuThrAspProGly | 32 | Qy |
| 3305 | 6 AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTATGAGTTTGGATCT | 324 | рь |
| 326 | AlaGluLysPhePheValSerValGlyLeuPrc | 311 | Qy |
| 3245 | ::: | 318 | Db |
| 310 | 1 IleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu | 29 | Qy |
| 3185 | 8AATAGAATATAATACTTGTTTAAATTTAAATTTACCTAAAAGTGAT | 313 | Дb |
| 290 | 1 TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn | 27 | Qy |
| 3137 | 1 ATAAGCCAATTAAATGAAGGTCCTCTTAACTCAAGAAATGTAAATATTTTGAATAAT | 308 | Db |
| 270 | 1 AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet | 25 | Qy |
| 3080 | | 304 | Db |
| 250 | GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn | 231 | Qy |
| 3044 | 2 | 301 | Db |
| 230 | ThrPhe | 21 | ν |
| 3011 | 5 GGATCTTTTAATGCCGGTGCAACTTTTGGAAGGTTTACGGGAAATTTCAATATAAAG | 295 | Db |
| 210 | TrpArgGlyAspTyrGluValAsn | 19 | Qy |
| 2954 | 4GAAATTCAATAAAAGGTTATGAGGATTTTGCCGTGATAAGTCCAATATTA | 290 | рь |
| 190 | 1 GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet | 17 | Qy |
| 2903 | | œ | Db |
| 170 | tAlaAsnSerLeuAspTyrAsnGluArgLeuT | 15: | ρy |
| 2882 | 8CCTGTTTCAACTGAA | 286 | Db |

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US-08-466-961A-16
                                                                                                                                      Sequence 16, Application US/08466961A Patent No. 5843709
                                  GENERAL INFORMATION:
APPLICANT: Entian
APPLICANT: G tz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4107
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             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATTCAAGATTATCTATTACCATTTATAACGGAATTAAAAGTTAATAATTTTATTAAT 3878
                                                                                                                                                                                                                                                                                                         ATTGGCAGTTTT---ATAAACATGCGTTGTAATAGAATATTCGGTATTAATCCT 4490
                                                                                                                                                                                                                                                                                                                                                                   AsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuGlyIleGlnPro 729
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTAGAAAATCTTAAAAAGGACACTACAAAAAAGCTTATATACTTCACGTTCTAGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGAAATTTTAAAAAAAGAATTTCCGAATCTTCATGAATTTCTATTTAATAAAATTAGT 4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAspIleIlePro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AAAAATTTATTAGCTAAACTT-------ACCAATCCTAAAAATGAC 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsnVal 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMet 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLys 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrpSer 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATCGTTGCT-----ATATCAATAGATTTTTTATTAGATTATTAGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeu 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCTATTA----TCAATAAATATAATACAATCAGAG---TTCAAAATTCCAAAAGAA 4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGlu 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCysGln 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATTTTTTACATAAAATTTAAAGAAGAT------GAAGATTTTATAAAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ArgThrGluValGluLysAlaIleArgMetSerArgSerArgIle 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ATTAATAAAAGTGAGAAAGAAGAAATTTTAATTAATAATGCG-----
Schnell, No. 5843709bert
                                     Entian, Karl-Dieter
G tz, Friedrich
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                 US-08-466-961A-16
                                                                                                                                                                                                        US-09-978-385-2 (1-805) x US-08-466-961A-16 (1-8700)
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                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Biosynthetic Process for the Preparation TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,625
2682 AAGCAATTGCTCTCAGATATAAATGGATTTGGCTATCCCAAAAAAGACAGTTATAGTTTT 2741
                                                                                                                                                                                                                                                                                                                                No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                  36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/784,234 FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                  1 MetSerSerSerSrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
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                                                                                                   IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu--
                                                                                                                                       ATTAGTGAAGCAGCATATATTCTCTGGTTATTATCTCCTAATCATTTTGGTACAAAAACT
                                                                  ATTAGGAATTATCACGAATTTTTTATGGATAAATATGGATTTGAACAACTAGTAAATTTA 2681
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1100 New York Avenue, NW
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Jung, G nther
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Kaletta, Cortina
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                              --AlaGluAspLeu-----PheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Matches:
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| Çī. | | 77 | Db |
|----------|--|------|----------------|
| 383 | isIleGlnTyrAspMet | 364 | Qy |
| 4 | : : : | 3426 | Db |
| 363 | leLeuMetCysThrLys | 344 | Qy |
| 3425 | ::: CTGACTCATTACCTTTTTGTCCAAGAATTATTATAAAAATATTATT | 3366 | В |
| 343 | | 338 | Qy |
| 3365 | TTTAAGAGAAATTTCATTTGAAAAAAAAATTTATACAACCTATA | 3306 | Db |
| 337 | MetLeuThrAspProGly | 327 | Qy |
| 3305 | AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTATGAGTTTGGATCT | 3246 | Db |
| 326 | ProAsnMetThrGlnGly | 311 | Qy |
| 3245 | | ω | Db · |
| 310 | leAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArqIlePheLvsGln | 291 | Qy |
| 3185 | - PATTAGATATATAATACTTGTTTAAATTTAAATTTACCTAAAAGTGAT | ω - | B 2 |
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| 770 | ATVTPTOSeTTVTT | 25 | O _V |
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| 250 | ysProLeuTyrGluHisLeuHisAlaTyrValArqAlaLysLeuMetAsn | 231 | Qy |
| 3044 | AAAGAAATAGTGCAT | 3012 | рь |
| 230 | llleGluAspValGluHisThrPhe | 211 | Qy |
| 3011 | GTGCAACTTTTGGAAGGTTTACGGGAAATTTCAATATAAAG | 2955 | Db |
| 210 | disTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn | 191 | Qy |
| 2954 | GGAAATTCAATAAAAGGTTATGAGGATTTTGCCGTGATAAGTCCAATATTA | 2904 | рь |
| 190 | yLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet | 171 | Qy |
| 2903 | TATAGTGAGATATATTT | 2883 | ф |
| 170 | SerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer | 151 | Qy |
| 2882 | | 2868 | ф |
| 150 | LeuAsnGlu | 131 | Qy |
| 2867 | AACGACGTTAAAAATTTAGAAAAGAATAATACAGTTTCTAAAAATCAATGCG | 2817 | Db |
| 130 | AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly | 111 | Qy |
| 2816 | TATTTGCTTGCAATTCAAAATAACAGCCATATTGAAATAACAGAA | 2772 | Db |
| 110 | 1LeuGlnGlnAsnGlySerSerValLeuSerGlu | 91 | Qy |
| 2771 | - | 2754 | Db |
| 90 | AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn | 71 | Qy |
| 2753 | TCTAATAACATT | 2742 | Db |
| 70 | AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer | 51 | Qy |

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Best Local Similarity:
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US-08-645-193B-18
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                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                              Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                      US-08-645-193B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESMODD, ROBERT W.
REGISTRATION NUMBER: 0652.1540000
REFERENCE/DOCKET NUMBER: 0652.1540000
REFERENCE/DOCKET NUMBER: 0652.1540000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ. ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08645193B
Patent No. 5962253
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: bot
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8700 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                           2562 ATTAGTGAAGCAGCATATATTCTCTGGTTATTATCTCCTAATCATTTTGGTACAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation
TITLE OF INVENTION: Catalyzed by Flavoprotein
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4440 ATTGGCAGTTTT---ATAAACATGCGTTGTAATAGAATATTCGGTATTAATCCT 4490
2622 ATTAGGAATTATCACGAATTTTTTATGGATAAATATGGATTTGAACAACTAGTAAATTTA 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 AsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuGlyIleGlnPro 729
                      21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu------
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ZIP: 20005
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                                                                                                               1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr
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| Ov 364 ValThrMetAspAspPheLeuThrAlaHisHisGluMetGlvHisIleGlpTvrAspMet 383 | ٧٥ | |
|---|------|-------------|
| Db 3426 TTAAAACCAGCTACTTGGAAAATAAATTCAGAAATGTTTTCTGAAACTGAA 3476 | Db 3 | |
| 344 CysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCy | Qy | |
| Db 3366 ACTGAAGAAGGCATTGACTCATTACCTTTTTGTCCAAGAATTATTATAAAAATATTATT 3425 | Db 3 | |
| 338 | Qy | |
| 3306 GAATTATACAAATTTTTAAGAGAAAT | Db 3 | |
| 327 | Qy | |
| Db 3246 AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTATGAGTTTGGATCT 3305 | рь з | |
| 311 | Qy | · · · · · · |
| Db 3186 ATAGATATAAATGACATATTTATTGGAGCTACATTTAACAAACTTTATCTATATTCTGAA 3245 | Db 3 | |
| 291 | Qy | |
| 3138AATAGAATATATAATACTTGTTTAAA | Db 3 | |
| 271 TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGl | Qy | |
| Db 3081 ATAAGCCAATTAAATGAAGGTCCTCTTAACTCAAGAAATGTAAATATTTTGAATAAT 3137 | Db 3 | |
| 251 | Qy | |
| Db 3045CATTACAATAATTACATGAATGAATGAATGGTTTAGAA 3080 | рь з | |
| 231 GluGluIleLysProLeuTyrGl | Qy | |
| Db 3012 3044 | Db 3 | |
| 211 GlyValAspGlyTyrAspTy | Qy | |
| Db 2955 GGATCTTTTAATGCCGGTGCAACTTTTGGAAGGTTTACGGGAAATTTCAATATAAAG 3011 | Db 2 | |
| 191 | Qy | |
| Db 2904GGAAATTCAATAAAAGGTTATGAGGATTTTGCCGTGATAAGTCCAATATTA 2954 | Db 2 | |
| 171 | Qy | |
| Db 2883 ATA 2903 | Db 2 | |
| 151 IleMetAlaAsnSerLeuAs | Qy | |
| Db 2868CCTGTTTCAACTGAA 2882 | Db 2 | |
| 131 | Qy | |
| Db 2817 AACGACGTTAAAAATTTAGAAAAGAATAATACAGTTTCTAAAATCAATGCG 2867 | Db 2 | |
| 111 | Qy | |
| Db 2772TATTTGCTTGCAATTCAAAATAACAGCCATATTGAAATAACAGAA 2816 | Db 2 | |
| 91 | Qy | |
| Db 2754 GCATTTTTAAAAGAAAAG2771 | Db 2 | |
| 71 | Qy | |
| 2742 | Db 2 | |
| Oy 51 AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer 70 | Qy | |
| 2682 | Db 2 | |
| Qy 36AlaGluAspLeuPheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50 | Qy | |

| 691 | ValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsnVal 6 | 672 | ρ |
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| 671 4280 | AI GOLITYI FIRELEULYS VALLYSASTGITMETILELEUP REGIYGIUGIUAS PVALATG (| 4272 | 8 8 |
| 651 4271 | ⊅ ⊏ | 4251 | S & 5 |
| 631 4250 | | 612 4203 | B 5 |
| 4202 | | 4202 | Вþ |
| 611 | ${\tt PheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrpSer} \ \ ($ | 592 | δ |
| 591 4202 | AsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeu :::: | 572 4158 | 유 성 |
| 571 4157 | GlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGlu : | 552 4107 | g V |
| 551 4106 | AlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAlaGly : ::::: | 532 4047 | ₽ 8 |
| 531 4046 | | 517 3987 | ₽ 8 |
| 516 3986 | CysaspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyr! | 498 3954 | B 8 |
| 497 3953 | TrpGluMetLysArgGluIleValGlyValValGluProValProHisAspGluThrTyr . :: | 478 3924 | Qy Db |
| 477 3923 | LysTrpArgTrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrp | 458 3879 | P S |
| 457 3878 | PheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGlu | 438 3819 | Qy Db |
| 437 3818 | SerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsn . | 420 3774 | Ωy db |
| 419 3773 | HisleuLys | 410 3714 | Db Qy |
| 409 3713 | GluGlyPheHisGluAlaValGlyGluIleMetSer | 398 3654 | Дy |
| 397 3653 | AlaGlnProPheLeuLeuArgAsnGlyAlaAsn ::: :: ATACTAAAAAAAGAACTAAAAAAAACATGGTAGGATTCGAATATTAGAAAGCTTTATCAAT | 387 3594 | g d |
| 386 3593 | AlatyralaAlatyralaAlatyrala | 3534 | gb Qy |
| 3533 | ::::: | 3477 | В |

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| rity: 47.78% Conservative: 12 34.44% Mismatches: 19 34.44% Indels: 18 4 Gaps: 18 2 (1-805) x US-09-280-116-114 (1-789) 3 (1-805) x US-09-280-116-114 (1-789) 2 (1-805) x US-09-280-116-114 (1-789) 3 (1-805) x US-09-280-116-114 (1-789) 4 (1-805) x US- | AAAAATTTATTAGCTAAACTTACCAATCCTAAAAATG AspileIlePro |
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-453-702B-1
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (608) 251-9:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6506
3628 GCAGGGAAAAACAAAATTAAACTTGCATTGCAAAAACCGGATAAAGTTACTTTGGCGTCCA 3569
                                                                                                                                                          3778 ACATTTATTCTCACACCGCCAGTAAGTCGTGTAGCAGGTGGTTCTGGCCCAACAACTTAAA 3719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION ONTA:
                                     65.AlaGly---AspLysTrpSerAlaPheLeuLysGluGlnSerThrLeu------ 79
                                                                                                                   45 LeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsn 64
                                                                                                                                                                                              25 AlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPheTyrGlnSerSer 44
                                                                                                                                                                                                                                                                            5 SerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThrIleGluGluGln 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Madison
                                                                              -----CTAAATGTTCTGGATATCCCTCCAAACAATCCACAAAAT 3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burland, Valer
Perna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plunkett, Guy
Welch, Rod
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120.50
32.57%
19.29%
2.81%
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608) 251-9166
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Indels:
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| 365 | 346 ProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCysThrLysValThr 3 | Qy |
|------|---|------|
| 2582 | 64 | Db 2 |
| 345 | nValGlnLysAlaV | Qy |
| | AATACTCTTTACCTGGAACATGGC | Db 2 |
| ω | -AsnSerMetLeuThrAspProGly | Qy |
| 2702 | 2761 GGCCGATTTAACAGTGGATTAAATTTATTTAGTTGGCAGTTACACTCTGATGCCAGCTAT 2 | Db 2 |
| 320 | 320 3 | Qy |
| 2762 | ngtcagtatcgctcttatgacagcaataataacagtaatacagccagttat | Db : |
| 320 | 318 ValGlyLeu | Qy |
| 2822 | CGCGGCATTGATGCTTTTATACCTCC | Дb |
| 317 | luLysPhePheValSer | Qy |
| 2867 | 2926 CACCGACTAAATTTAACAGTACCACAGGCGTATATCAATGAACTTGAAAGAGGTTACGTT: | Db |
| 299 | pValThrAspAlaMetValAsp | Qy |
| 2927 | AGTGGGATATCAGTGAA | DЪ |
| 287 | | Qy |
| 2987 | GAT | Db |
| 277 | rAsn | Qy |
| 3047 | - | DЪ |
| 261 | rIleSerProIleGlyCys | Qy |
| 3101 | AAATAAC | Db |
| 244 | isLeuHisAlaTyrVal | Qy |
| _ | TCAT | DЬ |
| 229 | ArgGlyGlnLeuIleGluAspVa. | Qy |
| 3194 | 3253 ATTTTTTGTATTCTTTTTCCGGGTTATGCTGAAGAAACTTTTGATACGCACTTTATGATC | Db |
| 209 | 194 AsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluVal | Qy |
| 2 | TGG | DЪ |
| 193 | 176 LeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMetAlaArgAla | Qy |
| 3314 | 3373 CACGCATCAGAATATGAACTAACGGTAGTTGATGATTACGGGAATAACATCCATAGTAAA | Db |
| 175 | Gln | Qy |
| ω | 3433 AATAATGAAAGTATCTTACTGCCTCCCTTTTCGCATAACGACATTACATTAAAAAATAAC | ДĎ |
| 155 | 138 ProGlnGluCysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSer | Qy |
| 3434 | 3475 TGGATAACGGTTACAACTATCAAAGCACAAAAACGTGAAAGTT | DЬ |
| 137 | LeuAsnThrMetSerThrIleTyrSerThrC | Qy |
| 3476 | ::: AAACAGCC | Db |
| 117 | GlnAsnGlySerSerValLeuSerGluAspLysSerLys | Qy |
| w i | TAAA | Db |
| 97 | 80 AlaGinMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeu | Qy |

| S rSerValAlaTyrAlaMetArgClnTyrPheLeuLysValLysAsnGlnMetIleLeuPh 665 | 0у 64 | |
|--|-------------------|-----|
| .7TATACTTTCTCTGC 1704 | Db 1717 | |
| 5 sSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPhe | Qу 62 | |
| 5 yTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysValArgIleSerLeuLy 625 | Qy 605 Db 1745 | |
| nTyrPheGluProLeuPheThTTpLeuLySASpGlnAsnLySAShSetFile****Valvi TTACTGGGGGCGAAGTGGAAATGCTAAAGATTACCAATTCAG 1 | Qy 586 Db 1787 | |
| TTATCCAATAATCTGGGAAATGTATCATTAAGTGCGCTTTTGGCGGAA 17 | щ | |
| rLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAs 586 | QY 567 | |
| TTATGATATTGGCAGAAAAAATAGCCTTTCTGCC | _ | |
| rThrGluAlaG | Qy 547 | |
| 7 uAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSe 547 : | Qy 527 Db 1934 | |
| ::: CACTCGATTTAGCGTGGCCCTGGCGTTATGCTTCGCAGGATTACAGGACATTCAGCGA 19 | Db 1994 | |
| 0 uTyrGlnPheGlnPheGlnG | Qy 520 | _ |
| TATAACACACGAAGGTACGAGCTATCAGGTCGCCTATAATAAATA | рь 2054 | _ |
| euPheHisValSerAsnAspTyr- | Qу 502 | _ |
| 7 lValGluProValPro | Qy 487 Db 2113 | |
| GAAATGGTTGGAAT | Db 2127 | |
| uIleProLysAspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyVa 4 | Qy 467 | _ |
| ACGATTTTATCCGATAACTATAATGCTATAACTCTGG | Db 2164 | _ |
| ThrLeu-PropheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGl 4 | Qy 449 | _ |
| ::: ::::::: GACTTTCTCGAGGCAAATTATATATATGGC | N | _ |
| AsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIle | Оу 432 | _ |
| ::: ::: 4 ATTTCAAATTTCGATTTTATCGCCGGACGCAGTAAGATATATGGTGTAAAGAATCAGGAG 2225 | N | _ |
| LeuLeuSerProAspPhe | Qy 423 | _ |
| AGTGTTCGTTCTTTTGGTGCCCTACTCTTCCGTGCCTACATGCTGCAACCTGGT 2 | N | |
| GluIleMetSerLeu | | ` |
| ASIGLIANASIGLUGLY | Qy 394 Db 2401 | - 0 |
| TCGCAAAATGGCTACATCATTTACCAAAAAGAGGTTCCCCCGGGACCATTTACTARCGCA | Db 2461 | |
| HisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArg 3 | Qy 374 | 0 |
| | Db 2521 | В |
| | | 0 |
| | Db 2581 | ы |

| | ., ., ., ., ., ., | | | RES US: S | Qу | Оу | Дy | Qу | Оy | Qy | Оу | Оу | Db |
|---|---|---|--|---|--|---|--|---|--|--|---|--|-------------------------|
| ETLING DATE: ATTORNET/AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB340P1 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 11384 base pairs TYPE: nucletc acid STRANDEDNESS: double | APPLICATION NUMBER: US/08/961,527 FILING DATE: CLASSIFICATION 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: | 2085 R REAR TYP M TYP TER: TING TING ABBT | DENCE ADDRES BE: Human (9410 Key (100 Key (110 Key (111 K | RESULT 18 US-08-961-527-45/c US-08-961-527-45/c Sequence 45, Application US/08961527 ; Sequence 45, Application US/08961527 ; Patent No. 6420135 ; GENERAL INFORMATION: APPLICANT: Charles Kunsch ; APPLICANT: Charles Kunsch ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences . NUMBER OF SEDUENCES: 391 | 800 pValGlnThr 803 ::: :: 1370 TATTAGTAGT 1361 | 780 oTyralaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAs 800 :: | 765 eArgAspArgLysLysAsnLysAlaArgSerglyGluAsn | 745 1PheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIl 765 ::: ::: 1505 TTATGGTATATAT | 725 uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa 745 1543 -GGAATTACTGGCATAGCCGGTGAACATGATCAGTTAAA 1506 | 705 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe 725 | 685 IThralaProLysasnValSerAspIleIleProArgThrGluValGluLysalaIleAr 705 :::: | 665 eGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheVa 685 | 1703 CAGCCAATCCTAT 1691 |

| SD. | T(| TOPOLOGY: linear -961-527-45 | |
|--|--|---|-----------|
| Align Pred. Score Perce Best 1 Query DB: | Alignment Sco Pred. No.: Score: Score: Percent Simi: Best Local S: Query Match: DB: | t Scores: 0.0142 | |
| us- | 09-97 | -385-2 (1-805) x US-08-961-527-45 (1-11384) | |
| D 09 | 23 11096 | GluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPheTyrGln 4 ::: GAAGCATTAAAAACCTTTATGACGGGTGAAAATTTTTATCTCCAA 1 | 2 1052 |
| dg Vy | 43 11051 | SerSerLeuAlaSer4 | 7 |
| Qy | 4.8 | TrpAsnTyrAsn | |
| Вþ | 10991 | | 0932 |
| Оу | 58 10931 | AsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSer | 0884 |
| ν | 78 | ThrLeuAlaGlnMatTvrProlanGlnTlnGlnTlnGlnTlnTrolanGlnTlnGlnTlnTrolanGlnTlnGlnTlnTrolanGlnT | 9 |
| DЬ | 10883 | AATATGGCTCAAGAAGGGCATATTTAC1 | 0857 |
| Qy | 95 | LeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGluAspLysSerLys 1 | .14 |
| рь | 10856 | AAATATCATGTCACACGTCAAAATGGTCATCAACTGATGAAG | 10815 |
| , O | 115 | ₽ | 34 |
| 5 | Ě | : | 0785 |
| P & | 135 | uGluProGlyLeuAsnGluIleMetAlaAsn 1 | 4 |
| QΨ | 15 | erlenaspuvrasnelnardenum | 86//8 |
| 라 | 10757 | GAGCTTCCTGAGAAGAAATGGAAGGA |)704 |
| Qy | 172 | ValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMetAla 19 | 21 |
| Db | 10703 | TGGGGCTTTGAAGAGCGTCCTGTC | 089(|
| γ | 19 | rgAl | щ |
| 6 | F/90T | AATATTTATGAAGTTCACGCTG |)641 |
| 7 Q |) N | ValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGlu 23 | 1 |
| 2 | , , | ISSCASICCTTATAGTTTTGCCCAGCTCAAGGATGAACTCATTCCTTATCTCGTT 1 | .0581 |
| y Qy | 23 | <pre>roLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAla 25 </pre> | Ä |
| Db | | AAATGAACTATACTCATATTGAG1 | 0557 |
| Qy | 25 | TyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrp 271 | μ |
|) D | ı o | TTTATGCCCTTGATGTCCCATCCTTTGGGCTTG | 518 |
| 3 8 | 27 | ArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysPro 28 | 9 |
| B | 10517 | GGTATCAGCTTATGGGTTACTTCGCTTTAGAGCATGCTTATGGCCGACCACACACTTT 10 | 70 |

| 556 | | 543 | Qy |
|-------|--|-------|----|
| 9565 | TATTTCGCTTCTCAGCTAAACCAGTTTTACAAAGA | N | Дb |
| 542 | HisLy | 540 | Qy |
| 9625 | AAATCTGAAGAACAGTTGGAATGGTCTAACCTAGAAGACCCAATGAATG | 9684 | Db |
| 539 | | 536 | Qy |
| 9685 | | 9744 | Db |
| 535 | CysGinAlaAlaLysHis | 530 | Qy |
| 9745 | | 9780 | DЬ |
| 529 | TyrSerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaL | 510 | Qy |
| 9781 | | 9840 | ДЪ |
| 509 | GluThrTyrCysAspProAlaSerLeuPheHisValSer | 495 | Qy |
| 9841 | B TTGCCATTCTCGCACGAT | 9858 | Db |
| 494 | | 475 | Qy |
| 9859 | 8 AAATATGACTTTAACCTGGTGACTTTCAGCTTTATGTATG | 9918 | Db |
| 474 | | 470 | Qy |
| 9919 | | 9978 | Db |
| 469 | | 459 | Qy |
| 9979 | 9 ATCAAGATTACGGGAATGAAAGAGATTGGTGGTCTAGGATTTGACTACAAA | 10029 | Db |
| 458 | LeuLeuLysGlnAlaLeu | 439 | Qy |
| 10030 | | 10071 | Db |
| 438 | LysSerIleGlyLeuLeu | 419 | Qy |
| 10072 | 0 TATTTCCTTCAGCGCTTGAATGAGGTTATTAAGTTAGAA | 10110 | Db |
| 418 | | 401 | Qy |
| 10111 | 8CCATGGACACCTAATAAAGATGGCGGAAATCTCAACTATGAAGGTTAT | 10158 | Db |
| 400 | 5 TyrAlaAlaGl | 38. | Qy |
| 10159 | 8 TIGGATGGTATICGIGIGGATGCTTAGCAACAIGCTCTATITIGGACTATGATGATGATGCT | 10218 | Db |
| 384 | | 370 | Qу |
| 10219 | 8 AAAAATGAAGTCCAGTCCTTC | 1027 | Db |
| 369 | 3 LysGlyAspPheArg | 35 | у |
| 10279 | GACCATAATAAGGCTCATAACCATGGTTGGGGTGCCCT | 10332 | Db |
| 352 | 8 AsnValGlnLysAlaValCysH | 33 | Qy |
| 10333 | TTACCATCAACGAT | 10391 | Db |
| 337 | LeuProAsnMetThro | 320 | Qy |
| | | 10406 | ДD |
| 319 | ${\tt GlnAlaTrpAspAlaGlnArgIlePheLys}$ | 300 | ОУ |
| | :: | 10457 | da |
| 299 | | 290 | ν |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08157171 Patent No. 5736323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                          TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9564 ACCAGCTATGATGGTATTGAAATCATTGATGCGGATAATCGAGACCAGAGTGTTCTTTCC 9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9444 GAGCGGAAAGATTTTACAATCGGACTACCCGTTGCAGGAATTTACGAAGAAGTATGGAAT 9385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9504 TTTATTCGTAAGGGTAAAAAGGGAGAAATGTTAGTCTGTATCTTTAATATGGTACCTGTT 9445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9261 GTATGGAAAATCAAACGTCGCTTGAAATCTACTAAAACCGTCACAAATAAAAAACCAAAAA 9202
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9201 GGAGTAGAAAATGAAAATGAAATGTTAGCTTTGAT 9166
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 GlnTyrPheLeuLys-----ValLysAsnGlnMetIleLeuPheGlyGluGluAspVal 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 TyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLysAla 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557 MetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAla 576
MOLECULE TYPE:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 ArgValAlaAsnLeuLysProArgIleSerPheAsn 682
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/157,171 FILING DATE: 24-JAN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 90 Soutn , CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Merchant & Gould STREET: 90 South 7th Street, 3100 No. 5736323west Center
                                     STRANDEDNESS:
                     TOPOLOGY:
                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAT---AATCAAACTGTTCAAACGCAAGAAGGACTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TGGAAAGATTATGAGCAGACCTTAACCTTTACCCTACCGGCTATGGGAGCAAGT 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMetArg 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGAGTTGGAAGAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysAsnMetAsnValArg-----ProLeuLeuAsnTyrPheGluProLeuPhe--- 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55402
                                                          nucleic acid
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Hubert, Christine
                     linear
DNA (genomic)
                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agents and Procedures for the Study of the Genetic Polymorphism of the Angiotensin I Converting
                                                                                                                                                                                                             8076.103USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TGGGGAGGCGTTTGGAAAGAA 9349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Percent Similarity:
Best Local Similarity:
                                 Score:
                                                 Pred. No.:
                                                             Alignment Scores:
                                                                                              US-08-961-527-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 115, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                             TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: Exon 17
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO::
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 LeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSer 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AACCAGGCTGCCCGGCTCAAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 TrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLys 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TGGCGAGACAAGGCGGGGAGAGCCATCCTCCAGTTTTACCCGGAAATACGTGGAACTCATC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: ASCII T
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CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                               STRANDEDNESS:
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nucleic acid
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| Qy 324 Db 2047 Qy 339 Db 1987 Qy 359 Db 1948 Qy 379 Db 1921 Qy 419 Db 1888 Qy 447 Db 1795 Qy 447 Db 1735 Qy 486 Db 1735 Qy 506 Db 1730 Db 1582 Qy 557 Db 1534 Qy 615 Db 1492 Qy 615 Db 1432 Qy 647 | OY 314 PHEPROVALSETVALGLYLeuProAshMet | 2131 ATAGACAGATTTGAAACAGAGAAA | Qy 294 ThraspalametValaspGlnalaTrpaspalaGlnargIlePheLysGlualaGluLys 313 | Qy 274 PheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 ::: | 2206 | QY 254 SerTyrTleSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | Db 2224TTGACTGGTTCAACACCC 2207 | 2263 GGGCATGATTATAGAGGAGCAATCAGAGATTTTTACCAT | 214 GlyTyrAspTyrSe | QY 204ArgGLyAspTyrGluValAsnGlyValAsp | 2377 ATTATT | 184 | | 2494 AAAGGAAATTITGCCGTATATGGTAGTCGCTGGTATTTTGGTGAATCTATTGAAACGTTA | Oy 132 ValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151 Db 2524 TTTAACGCCGAAAAATTJATTTATAGAATTA 2495 | Db 2584 ACATCAAACGTACTAGATATTATGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 | 117 | :::::: : ::: 2644 AGAACGACAACTTATCTATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG | 112 | | Db 2746 GAAAACAAATTGAAAATTTTTAAGGGAGAGTTTTATCGAATCTCTGTATTA 2696 | Qy 76 GlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsnLeu 91 | 2800 ATGAAAAACGCATCAAAAATGGTGCGTTCTGTTTTTATGCTACCATAAAAGGAG | 59 | Qy 40 PheTyrclnSerSerLeuAlaSerTrpAsnTyrAsnThr~AsnIleThrGluGluAsn 58 | -09-978- | Query Match: 2.80% Indels: 298 DB: 4 Gaps: 42 |
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| .nTyrPheLeuLysValLysAsnGlnMetIle 663 | TyrP | 64 | Qy |
|---|------------------------------------|----------|----|
| TCCTTTTAATAGTAAAGAACCTTGGTTTTTTTCAGAAAC | 2 CGATTACATAGTTCTAGAAGTCCTT | 143 | ДD |
| rGluTrpAsnAspAsnGluMetTyrLeuPheArgSer | AlaLeuGlyAspLysAlaTyr(| 627 | γQ |
| AACTAG | 2 GATTATGACGAAGAGCTACAAACTAGA | 149 | Db |
| ·sValArg | AspGlnSe | 615 | Qy |
| TGGAGTCATG | | 152 | ΔQ |
| lGlyTrpSerThrAspTrpSe | AspGlnAsnLysAsnSerPheVal(| 597 | VΩ |
| TATAGTTGG 1526 | | 153 | ΔŒ |
| oLeuLeuAsnTyrPheGluPro | Ĺe | 57 | νg |
| CAACCCTATTTTACAGCGACAGCATCTAATATCGGT 1535 | - | 158 | Db |
| erGluProTrpThrLeuAlaLeuGluAsnValValGlyAla 576 | uArgLeuGlyLys | 55 | Qγ |
| STTTTTCAGGGGATACTATTATTAGTTGGAAT 1583 | 3 AGTCACCGCTACCCTGTTGGTTTTCA | 163 | ДĎ |
| ThrGluAlaGlyGlnLysLeuPheAs | 9 LeuHisLysCysAspIleSerAsnSerTh | 53 | Qy |
| CAGGATAGTTGTAAAAATGCAGAAGGTGGTTTGATTTTATCAAGATATGCAGGTCCTGGT 1634 | 3 CAGGATAGTTGTAAAAATGCAGAAG | 169 | Db |
| la | 6 GlnGluAlaLeuCysGlnAla | 52 | Qy |
| TGGCTTTTAAACCATTATCACTAT 1694 | | 1717 | Db |
| <pre>IleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPh</pre> | leA | 50 | Qy |
| 1718 | i | 173 | ДD |
| coHisAspGluThrTyrCysAspProAlaSerLeuPheHis 505 | LuProValProHis | 4.8 | Qy |
| CAGGGAGTAGATTTTTGGTGGATTGACTGGCAACAAGGGACACAA 1736 | 0CAGGGAGTAG | 178 | Дb |
| cpMetLysLysTrpTrpGluMetLysArgGluIleVal 485 | 7 GlulleProLysAspGlnTrpMetL | 46 | QΥ |
| TATGAACTAGAAAAG 1781 | 5TATG | 179 | DЬ |
| nrTyrMetLeuGluLysTrpArgTrpMetValPheLysGly 466 | 7 ValGlyThrLeuProPheThrTyrM | 44 | Qy |
| TTAAAGATGTTCAT 1796 | 8 TCTTTTAGGGAAGCCTACTTTAAAGATGTTCA | 182 | 맖 |
| luThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIle 446 | 7 AspPheGlnGluAspAsnGluThrG | 42 | Qy |
| ACTAGAAGAACCTGCTATTTTGATTTTTTAATCC | 8 AAACGGTTGGGGTTAAATGTAGAAC | 188 | Дb |
| LeuSerp | LysSerIleGlyLeu | 419 | Qy |
| | 1 | 190 | Дb |
| lyGluIleMetSerLeuSerAlaAlaThrProLysHisLeu 418 | GlyPheHisGluAlaValGlyGluI | . 399 | Qy |
| AT 1901 | CTTAT | 192 | Db |
| yrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGlu 398 | spMetAlaTyrAlaA | 37 | Qy |
| TTAAATGTCCATCCTGCTGATGGGATA 1922 | 1 | 194 | Db |
| lThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHis 378 | 9 LeuMetCysThrLysValThrMetA | <u>ω</u> | Qy |
| AAAGCTAAAACTCTCC | 7 TTATTGCAACAACTTCATGATAG | 198 | Db |
| isProThrAlaTrpAspLeuGlyLysGlyAspPheArgIle 358 | CysHis | 33 | ογ |
| AGGATATAGTTGGAATAGAAACTTAATACCAAATCCAGAACAG 1988 | 7 TTTGGAAGTGGCTGGACAGGATATA | 204 | DЬ |
| lnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsn 338 | | 324 | Qy |

Db 1372 ACATCTAAGATTATGAAGAAATAC---CTTCGTTTGAGACATCAGATGATT 1325

Search completed: March 7, 2003, 09:50:13 Job time : 166 secs

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Command line parameters:

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-O_-GGD2_1/USPTO_Spool/US09978385/runat_28022003_104718_1445/app_query.fasta_1.967
-OB-PUD11shed_Applications_NA -QFMT=fastap -SUFFIX-p2n.rnpb -MINMATCH=0.1
-LOOPEX-0 -UNITS-bits -START=1 -END-:1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-20 -MODE-LOCAL -OUTFMI-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN-200000000 -USER-US09978385_@CGN_1 1_80_@runat_28022003_104718_1445
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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ALIGNMENTS

| pplicati 20020177 MAATION: iddingto petrie, Shoemake Bishoemake Bishoemake CE: 99-2 ICATION: DATE: ATION NU DATE: 1 ATION NU DATE: 1 ATION NU DATE: 2 Q ID NOS StSEQ fo 4 omo sapi DS 35)(2 | Sequence 1, Application US/09978385 Patent No. US20020177211A1 GENERAL INFORMATION: APPLICANT: Piddington, Christopher S. APPLICANT: Shoemaker, Kimberly E. APPLICANT: Shoemaker, Kimberly E. APPLICANT: Bishop, Paul D. TITLE OF INVENTION: ZACE: A HUMAN METALLOENZYME FILE REFERENCE: 99-24C1 CURRENT APPLICATION NUMBER: US/09/978,385 CURRENT FILING DATE: 2001-10-16 PRIOR APPLICATION NUMBER: 60/133,952 PRIOR FILING DATE: 1999-08-27 PRIOR FILING DATE: 1999-08-27 PRIOR APPLICATION NUMBER: 60/151,181 PRIOR PILING DATE: 1999-08-27 PRIOR APPLICATION NUMBER: 09/563,516 PRIOR FILING DATE: 2000-05-03 NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0 ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (35)(2449) | ; NAME/KEY: ; LOCATION: | ; TYPE: DNA ; ORGANISM: | ; LENGTH: 3334 | ; SEO ID NO | ; NUMBER | ; PRIOR F | ; PRIOR A | ; PRIOR F | ; PRIOR A | ; PRIOR F | ; PRIOR A | ; CURRENT | ; CURRENT | ; FILE RE | ; TITLE O | ; APPLICANT: | ; APPLICANT: | ; APPLICANT: | ; APPLICANT: | ; GENERAL | ; Patent No. | ; Sequence | US-09-978-385-1 | |
|--|--|-------------------------|-------------------------|----------------|-------------|---------------|----------------|---------------|----------------|----------------|-----------|---------------|--------------|-------------|---------------|---------------------|--------------|--------------|--------------|--------------|----------------------|---------------|--------------|-----------------|--|
| | on US/09978385 211A1 211A1 n, Christopher Charles r, Kimberly E. Paul D. ZACE2: A HUMAN 4C1 2001-10-16 999-08-27 MBER: 60/131,18 999-08-27 000-05-03 : 11 000-05-03 : 11 mindows Versi ens | | Homo | 3334 | ٠٠ سر | OF SEQ ID NOS | FILING DATE: 2 | PPLICATION NU | FILING DATE: 1 | APPLICATION NU | | PPLICATION NU | FILING DATE: | APPLICATION | FERENCE: 99-2 | TITLE OF INVENTION: | | | | | GENERAL INFORMATION: | o. us20020177 | 1, Applicati | 385-1 | |

Score:
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| | euPheArgS | leSerLeuL TAAGCCTAA | erPheValG CTTTTGTGG | rgProLeuL GGCCACTGC | | FG - SA | InPheGlnP AATTCCAGT | erLeuPheH CTCTGTTCC | | etValPhel TGGTCTTTA | InAlaLeuT | lyLeuLeus | SLUALAVALO SAAGCTGTTG | SPMETALAT | hrLysValT | laValCysE | snMetThro | |
| heGlyGluG | erSerVal <i>l</i> | ysserAlaI AATCAGCTC | lyTrpSer] GATGGAGT <i>I</i> | euAsnTyrF !TCAACTAC! | roTrpThrI | erAsnSer1 | heGlnGlu !TTCAAGAA(| lisValSer! ATGTTTCT/ | /alGlyVal\ !TTGGGGTG | Jysgiygiu AAGGGGAAJ | hrIleValo | BerProAspI | SlyGluIle GGGAAATC | TyrAlaAla ATGCTGCA | ThrMetAsp | isProThr. | BlnGlyPhe' BAAGGATTC | HIIIIIII DAGAGAATA |
| luAspVal | laTyrAlaI CATATGCT | JeuGlyAsp TTGGAGAT | ThrAspTrp: ACCGACTGG | PheGluPro TTGAGCCC | LeuAlaLeu TAGCATTG | ThrGluAla ACAGAAGCT | AlaLeuCys CACTTTGT | ASDASPTYr AATGATTAC | ValGluPro | ILEProLys | GlyThrLeu | PheGlnGlu | MetSerLeu ATGTCACTT | GinProPhe | AspPheLeu | AlaTrpAsp GCTTGGGAC | TrpGluAsn TGGGAAAAT | TTCAAGGAG |
| \rgValAla | | LysalaTyr AAGCATAT | SerProTyr. AGTCCATAT | roLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys | rGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn | 31yGlnLys GACAGAAA | GlnAlaAla CAAGCAGCT | SerPhelle CATTCATT | ValProHis GTGCCCCAT | alPhelysGlyGluILeProLysAspGlnTrpMetLysLysTrpTrpGlnMet | Alberthr IleValGlyThrLouProPheThrTyrMetLeuGlluySTrpArg | euLeuSerProAspPheGinGluAspAsnGluThrGluIleAsnPheLeuLeu | SerAlaAla TCTGCAGCC | LeuLeuArg | ThrAlaHis | alCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeumet | etThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | |
| AsnLeuLys | TyrPheLeu aCTTTTT | GluTrpAsn GAATGGAAC | AlaAspGln GCAGACCAA | TrpLeuLys GGCTGAAA | ValGlyAla GTAGGAGCA | LeuPheAsn CTGTTCAAT | LysHisGlu AAACATGAA | ArgTyrTyr CGATATTAC | AspGluThr GATGAAACA | MetLysLys ATGAAAAAG | TyrMetLeu TACATGTTA | ThrGluIle | ThrProLys | ASNGlyAla AATGGAGCT | HisGluMet | GlyAspPhe GGCGACTTC | ThraspPro | TTCTTTGTA |
| eLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer | LysvalLys | erLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet | heValG1yTrpSerThrAspTrpSerProTyrAlaAspG1nSerI1eLysVa1 | AspGlnAsr GACCAGAAC | LysasnMet | <pre>splleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu </pre> | heclnPheclnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis | euPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | .ulleValGlyValValGluProValProHisAspGluThrTyrCysAspPro | TrpTrpGL | GAGAAGTG | ASnPheLet | .laValGlyGluIIEMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | etAlaTyrAlaAlaGinProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe - | ysValThrMetAspAspPheteuThrAlaHisHisGluMetGlyHisIleGlu | ArgileLe AGGATCCT |)GlyAsnVa GGAAATGT | TCTGTTGG |
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APPLICANT: Jacobs, Kenneth
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APPLICANT: Genetics Institute, Inc.
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
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CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
EARLIER FILING DATE: 1999-10-06
NUMBER: Patentin Ver. 2.0
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                                        US-09-978-385-2 (1-805) x US-10-114-893-85 (1-3325)
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                                                                                                                                         GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer
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                                                                                              PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal
                                                                                                                              CAGATGATTCTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC
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                                        GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC
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Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
     PRIOR
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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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OR APPLICATION NUMBER: 60/049911
OR FILING DATE: 1997-06-18
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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Stewart, Timothy
Tumas, Daniel
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Sherwood, Steven
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COR PILING DATE: 1997-11-03
COR APPLICATION NUMBER: 60/064809
COR PILING DATE: 1997-11-17
COR APPLICATION NUMBER: 60/065186
COR FILING DATE: 1997-11-12
COR APPLICATION NUMBER: 60/065845
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COR APPLICATION NUMBER: 60/066364
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COR APPLICATION NUMBER: 60/066364
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COR APPLICATION NUMBER: 60/066364 FILING DATE: 1998-02-04 APPLICATION NUMBER: 60/0 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/0 APPLICATION NUMBER: 60/069694 FILING DATE: 1997-12-16 APPLICATION NUMBER: 60/072320 APPLICATION NUMBER: 60/069212 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069278 FILING DATE: 1997-12-11 FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/063735
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APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063045
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063082
FILING DATE: 1997-10-31 FILING DATE: APPLICATION NUMBER: 60/063329 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063327 APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24 1998-03-27 1998-04-09 NUMBER: 60/081229 NUMBER: 60/079663 1998-02-27 1998-03-25 1998-03-20 1998-03-31 1997-11-24 1998-01-23 1997-10-60/081203 60/074092 60/080165 60/077791 60/079294 60/078910 60/074086 60/073612 60/069334 60/066511

PRIOR PRIOR PRIOR PRIOR OR APPLICATION NUMBER: 60/088730
OR APPLICATION NUMBER: 60/088730
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088741
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 19/98-06-11
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
OR APPLICATION NUMBER: 60/089599
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
OR APPLICATION NUMBER: 60/089599 OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090349
OR FILING DATE: 1998-06-23
OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24 DR FILING DATE: 1998-05-13

OR APPLICATION NUMBER: 60/085338

DR FILING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/085339

DR FILING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/085579 DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084637
DR APPLICATION NUMBER: 60/085149
DR APPLICATION NUMBER: 60/085149
DR FILING DATE: 1998-05-12
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/086414 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/086430 FILING DATE: 1998-05-APPLICATION NUMBER: 60/ FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/083545 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: FILING DATE: 1998-0 FILING DATE: 1998-04 APPLICATION NUMBER: APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-14 FILING DATE: 1998-04-29 FILING DATE: 1998-04момвек: 60/084600 : 1998-05-07 1998-07-0 1998-04-1 60/091519 60/091360 60/090538 60/081818 60/081817 60/082999

| 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLys | GINGCITY:FOLEUGIG:GULTEGIDASCHEUTERVALLY | 8-385-2 (1-805) x US-10-028-072-71 (1-3732) MetSerSerSerSerFrpLeuLeuSerLeuValAlaVallililililililililililililililililil | 0 Length: 4142.00 Matches: 85.33% Conservative ity: 85.23% Mismatches: 96.53% Indels: 9 Gaps: |
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| YLYSGINLEUARGPROLEUTYT 180 | | rhralaalaGlnSerThr 2 | 3732 802 e: 1 138 |

| 2019 GTCAAAGAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 2078 | Db |
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| 555 555 | Qy |
| 1959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018 | Db |
| 555 555 | Qy |
| 1899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | DЪ |
| 555 555 | Qy |
| 1839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG | Дb |
| 555 555 | Qy |
| 1779 ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838 | Дb |
| 555 | Qy |
| 1719 AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778 | Db |
| 555 | Qy |
| AG? | Db |
| ysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLe | Qy |
| | Db |
| ${\tt yrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuch}$ | ОУ |
| 1540 GCATCTCTGTTCCCATGTTTCTGATGATTACTCATTCATT | Db |
| laSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThr | Qy |
| GTGACCC | Db |
| ArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspP | Qy |
| 1420 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1479 | Db |
| ${\tt rpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGlup} \\$ | Qy |
| 1360 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTAC | Db |
| GlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTı | Qy |
| 1300 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1359 | Db |
| VLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeu | Qy |
| 1240 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACCCTAAGCATTTAAAATCC 1299 | DЬ |
| isGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSe | Qy |
| 1180 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1239 | Db |
| yrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsn | Qy |
| TCCA | DЪ |
| ysThrLysValThrMet | Qy |
| 1060 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1119 | Db |
| laValCysHisProThrAlaTrpAspLeuGlyLysGly | Qy |
| 1000 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1059 | Db |
| roAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValG | Qy |

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GENERAL INFORMATION:
APPLICANT: Baker, Kevi
APPLICANT: Beresini,
APPLICANT: DeForge,
APPLICANT: Desovyers
APPLICANT: Desovyers
APPLICANT: Gao, Wei-
APPLICANT: Gao, Wei-
APPLICANT: Gerritser
APPLICANT: Goddard, J.
APPLICANT: Godowski
APPLICANT: Godowski
APPLICANT: Gurney, Au
APPLICANT: Smith, Vic
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Filvaroff, Ellen
Gao, Wei-Qlang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 71
LENGTH: 3732
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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CURRENT FILING DATE: 2002-04-12
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                              GATTATTGGAGAGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC
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Wood, William
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APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desovers, Luc
APPLICANT: Desovers, Luc
APPLICANT: Geo, Wei-Qiang
APPLICANT: Georitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy
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; ORGANISM: Homo
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US-10-123-904-71
Sequence 71, Application US/10123904
Publication No. US20030022328A1
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 71
LENGTH: 3732
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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CURRENT FILING DATE: 2002-04-16
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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                                  gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe
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                                                                                                                                                                                                                                     SEQ ID NO 71
LENGTH: 3732
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| ysHisLeuLysSer 42 | 381 TyraspMetAlaTyralaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400 | PheLeuThralaHisHisGluMetGlyHisIleGln 3 | JILeLeuMet 3 SATCCTTATG 1 | 321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340 | 301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320 | 80 TTGACAGTTCCCTTTGGACA | 20 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 87 | ysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeu | 60 CATGCCTATGTGAGGGCAAAGTTGATGATGATGCCTATCCTTCCT | 41 HisAlaTyrValArqAlaLysLeuMetAsnAlaTyrProSerTyrT]eSerProT]eGly 26 | | 1 GlnLeuIleGluAspValGluHisThrPheGluGluIleLvsProLenTvrGlnHisLen 24 | 20 ASPYYLIEPHYGAYASPIYYGAUWALASHGAYVALASPGAYTYRASPTYYSGARAGGIY 220 | 01 AspTvrTrDArd()vAspTvrf();ValAspCl;V-1,10-1,10-1,10-1,10-1,10-1,10-1,10-1,1 | JGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 20 | 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180 | 141 CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160 | 121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140 | 101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120 | 81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100 | 61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80 | |
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| 625 sSeralaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe 645 | 606 TrpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy 625 | 98 7 | 566 TrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeu 585 | 556AsnMetLeuArgLeuGlyLysSerGluPro 565 [| 19 GTCAAAGAGAAAGCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 2 | 1959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018 | 1899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | 555 555 | 1839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG | 555 555 | 1779 ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838 | 555 555 | 1719 AAATGITGAACCFCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778 | 555 555 | 541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe | 521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540 | 01 AlaSer 40 GCATCT | 80 | ol TrpMet 20 TGGATC | 41 LysGinAlaLeuThrILeVaiGLyThrLeuProPheThrTyrMetLeuGluLysTrpArg | | GAA Gly |

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                                                                       SEQ ID NO 71
                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin APPLICANT: Beresini, Ma
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NUMBER OF SEQ ID NOS: 550
                                                                                                       CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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                                                                                                                 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly
                                                                                                                                          CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT
                                                                                                                                                  GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
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AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu
                                                                                                        AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT
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Matches:
Conservative:
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| 565 | AsnMetLeuArgLeuGlyLysSerGluPro | 556 | Σ¥ |
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| 2078 | GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGA | ï | , ₽ |
| 555 | | 555 | Ϋ́ |
| 2018 | GTTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA | 1959 | 8 |
| 555 | | 555 | ¥ |
| 1958 | TTCTCCCTATCATAACTACAGCCCTCTCTTCC | 1899 | 8 |
| 555 | | 555 | Ą |
| 1898 | CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG | 1839 | 8 |
| 555 | | 555 | Ŋ |
| 1838 | ATTTCTTTGTTCTAAAAAGAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA | 1779 | 용 |
| 555 | | 555 | Ş |
| 1778 | AAATGTTGAACCTCCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG | 1719 | ᄝ |
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| 555 1718 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe | 541 1660 | 유 상 |
| 1659 | TACCAATTCC | 0 1 | 무 첫 |
| · in | GCATCTCTGTTCCATGTTTCTGATGATTACTCATTCATTC | 1540 | 문 |
| 520 | AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | 501 | Ϋ́ |
| 500 1539 | L LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro | 481 1480 | ₽ 8 |
| 480 1479 | TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | 461 1420 | ₽ 5v |
| 460 1419 | L LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 441 1360 | P Q |
| 440 1359 | IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 1300 | ρ 2 |
| 420 1299 | HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | 401 1240 | 유 정 |
| 400 1239 | TyraspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe | 381 1180 | B & |
| 380 1179 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln | 361 1120 | β Q |
| 360 1119 | LysalaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgTleLeuMet | 341 1060 | β δ |
| 340 1059 | ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | 321 1000 | D Qy |

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Sequence 71, Application US/10176918
Publication No. US20030027275A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qlang
APPLICANT: Gao, Wei-Qlang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
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APPLICANT: Sherwood, Steven
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Ensoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Geritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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NUMBER OF SEQ ID NOS: 550

SEQ ID NO 71

LENGTH: 3732

TYPE: DNA

ORGANISM: Homo Sapien
US-10-176-918-71
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C382

CURRENT APPLICATION NUMBER: US/10/176,918

CURRENT FILING DATE: 2002-06-20
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                                                                                                                                                                      ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
                                                        AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
                                                                                                              GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
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                                          GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC
                                                                                                 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG
                                                                                                                                                         AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT
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Wood, William
Zhang, Zemin
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Matches:
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| 1838 | APTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | 1779 | 了 |
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| 555 | | 555 | Qy |
| 1778 | AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG | 1719 | Дb |
| 555 | | 555 | Qy |
| 555 1718 | LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe | 541 1660 | . Db |
| 540 1659 | TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis | 521 1600 | Qy Db |
| 520 1599 | ArgTyrTyrThrArgThrLeu CGATATTACACAAGGACCCTT | 501 1540 | Фр |
| 500 1539 | ValValGluProValProHisAspGluThrTyrCysAspPro | | Qy Db |
| 480 1479 | MetLysLysTrpTrpGluMet TGAAAAAGTGGTGGGAGATG | 461 1420 | Qy Db |
| 460 1419 | LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 441 1360 | Qy Db |
| 440 1359 | IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 1300 | Qy Db |
| 420 1299 | HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | 401 1240 | Qy Db |
| 400 1239 | TyraspMetalaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe | 381 1180 | Qу Дъ |
| 380 1179 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln | 361 1120 | Оу |
| 360 1119 | LysalaValCysHisProThralaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet | 341 1060 | Оу |
| 340 1059 | ProAssMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | 321 1000 | ДУ |
| 320 999 | AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu | 301 940 | Qy Db |
| 300 939 | LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln | 281 880 | Qy Db |
| 280 879 | CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer | 261 820 | Qy Db |
| 260 819 | HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly | 241 760 | Оу |
| | TTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT | 0 | Db |

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                                    TATTAGCAAAGGAGAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTT
                                              pIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPh 805
                                                                             CAGAGATCGGAAGAAGAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGA
                                                                                       eArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAs 785
                                                                                                                    TTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGAT
                                                                                                                              lPheGlyValValMetGlyValI1eValValGlyI1eValI1leLeuI1ePheThrGlyI1 765
                                                                                                                                                            CACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAG
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                                                                                                                                                                                                                                                                                      sSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe
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APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laur
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-olan
APPLICANT: Gaodard, Audr
APPLICANT: Goddwski, Pau
APPLICANT: Godowski, Pau
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GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu
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                                                            CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA
                                                                                                                   CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT
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                                                                                                                                                                                           AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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| 520 | . AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | 501 | Qy |
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| | TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGAT | N N | g |
| 4 6 | TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | 46 | , Qy |
| 460 141 | LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 441 1360 | DP QA |
| 13 | . IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 | Qy |
| | | 1300 | Db |
| 420 | H1SGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrPa | 401 | Оу |
| 129 | | 1240 | |
| 400 | TyraspMetAlaTyralaAlaGlnProPheLeuLeul | 381 | Фр |
| 123 | | 1180 | |
| 380 | CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisII | 361 | Ор |
| 117 | | 1120 | |
| 360 | LysalaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspP} | 341 | Qу |
| 111 | | 1060 | ДЪ |
| 340 | ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnVal | 321 | Qу |
| 105 | | 1000 | |
| 320 | . AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu | 301 | ОУ |
| 999 | | 940 | |
| 300 939 | 4 – F | 281 880 | DP 6A |
| 280 | CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer | 261 | Оy |
| 879 | | 820 | |
| 260 | HisalaTyrValArgAlaLysLeuMetasnAlaTyrProSerTyrIleSerProIleGly | 241 | Qy |
| 819 | | 760 | |
| 240 | GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu | 221 | Qу |
| 759 | | 700 | |
| 220 699 | AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly | 201 640 | ФФ |
| 200 | GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHiSTyrGluAspTyrGly | 181 | ду |
| 639 | | 580 | |
| 180 | ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr | 161 | Qу |
| 579 | | 520 | Дъ |
| 1 6 | MetAlaAsnSerLeuAspTyrAsnGlu ATGGCAAACAGTTTAGACTACAATGAG | 141 460 | Дy |
| ` | | | |

| luPheLe 725 AGTTTCT 2617 | gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGl | 705 2558 | Qy |
|--|--|----------------------|----------|
| 1aIleAr 705 CCATCAG 2557 | ThralaProLysasnValSerAspIleIleProArgThrGluValGluLysAl | 685 2498 | Оу |
| hePheVa 685 TCTTTGT 2497 | eGlyGluGluAspValArgValAlaAssnLeuLysProArgIleSerPheAssnPh | 665 2438 | Qy Db |
| leLeuPh 665 TTCTTTT 2437 | rSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIl | 645 2378 | Qy Db |
| heArgSe 645 TCCGATC 2377 | SSETAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPh | 625 2318 | Qy Db |
| erLeuLy 625 CCTAAA 2317 | TrpSerThraspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSe | 606 2258 | Qy Db |
| eValGly 605 } GTGGGA 2257 | ASNTYPPheGluProLeuPheThrTrpLeuLySASpGlnASnLySASnSerPhe | 586 2198 | Qy Db |
| OLeuLeu 585 ACTGCTC 2197 | TrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgPro | 566 2139 | Qy Db |
| rGluPro 565 AGAACCC 2138 | AsnMetLeuArgLeuGlyLysSer | 556 2079 | Qy Db |
| CCTCAA 2078 | ATATGTACATCTGGAACC | 2019 | Db |
| 555 | | 555 | Qy |
| TAGCCAA 2018 | GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTT | 1959 | Дb |
| 555 | | 555 | Qy |
| GGTTTAG 1958 | TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | 1899 | Db |
| 555 | | 555 | Qy |
| œ | ATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACTAGGTGGGCC | ũ | Db 3 |
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| AACCAAA 1838 | AAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 1770 | , Y |
| TATTTG 17 | ATGCCTAGGTTTG | \vdash | рь |
| 55 | | 555 | Qy |
| FACCTCA 1718 | LysCysAspIleSerAsnSerThrGluAlaGLyGlnLysLeuPne | 5 4 1 1660 | Оу |
| n 6 | CANGANGCACIIIGICANGCAGCIANACAIGANGCC | TOU | מט |
| ProLeuHis 540 | TyrGlnPheGlnPheGlnAlaLeuCysGlnAlaAlaLysHisGluGlyPro | N | , Oy |
| ACCCTT 1599 | | 1540 | Db |

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; LENGTH: 3732
; TYPE: DNA
; ORGANISM: HOMO 9
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                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                          Local Similarity:
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Gerritsen, Mary E.
Goddard, Nudrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
smith, Victoria
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Filvaroff, Ellen
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                                                         TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe
                                                                                                        CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln
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          SSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe
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| MetThr | GATGCA | spAla | alPro | ProAla CTGCT | LaTyrVal CTATGTG | leGlu - - TTGA/ | rpAi | TYTVal | TrpAla !recect | euLe - - TAC | MetSer | lnAsnGly CAAAATGGG | YIPI ATCC | AsnAsnA AATAATG | SerSerL AGTTCAC | GluGln: GAACAG | SerSer | (1-805 | ty: arity: |
| GlnGly | CAGAGAAT | - = | PheGly | HisLeu CATTTG | Argāla ;AGGGCA | AspVa SATGT | gglyAsp ;AGGAGAC | 1ValLeu GGTCTTG | TrpGlu TGGGAA | euGluPro TGAACCA | ThrileT | SerSer | OLeuGlnG !ACTACAAG | AlaGlyA CTGGGG | euAla TTGCT | 6 - P | FICCTGG |) x US | 4142 85.3 85.2 96.5 |
| PheTrp | ATTC | ePhe | yGlnLysP ACAGAAAC | roAlaHisLeuLeuGly CTGCTCATTTGCTTGGT | AlaLysLeu CAAAGTTG | lGluHis GGAACAT | ASPTYrGluVa GACTATGAAG | euLysAsn GAAAAAT | SerTr AGCTG | roGlyLeuAsnGluIl CAGGTTTGAATGAAAT | yrSer ACAGT | erValLeu CAGTGCTC | luile AAAT | AspLysTr GACAAATG | SerTr | aLysThrPheLeuAspI CAAGACATTTTTGGACA | rTrpLeuLeuL TGGCTCCTTC | -10-14 | * * * * 0 |
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| nSerMe | GCCGA | AlaGl | IleA: ATAG | tTrpGlyAr | nAlaTyrp: GCCTATC | eGluGluIleI TGAAGAGATTI | nGlyValAsı GGGGTAGA | tAlaArgAl: 3GCAAGAGC | rGluValGlyI GAGGTCGGC | 2 - B | hrGlyLysVa CTGGAAAAGT: | uAspLysSe AGACAAGAG | CIC | rAlaPho TGCCTT | Asn AAC | pLysPheAsnF | rLeuVa CCTTGT | -71 (1 | Matcher Conserv Mismato Indels Gaps: |
| tLeuThr | GAAGTTC | Lysi | spValThrA ATGTTACTG | yArgPher ragaTTTT | 걸=; | 5-2 | 7 - 2 | <u> </u> | 2-5 | MetAlaAsn \TGGCAAAC | AlCysAsn TTTGTAAC | sSerLysa aGCAAAC | ThrValLysI ACAGTCAAG | PheLeuLysG] TTTTAAAGG! | ThrasnIleThrGluG ACCAATATTACTGAAG | eAsnHis AACCAC | ValAlaValT} STTGCTGTAAC | -3732) | ss: vative ches: |
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| vsSerGluPro 565 | 6BsnMetLeuArgLeuGlyLysSerGluPro | 55 | Q |
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| SAACCCCTCAA 2078 | 9 GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTC | 2019 | 망 |
| 555 | | 55 | Qy |
| AATTTAGCCAA 2018 | 9 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCC | 1959 | Db |
| 555 | (J) | 55 | Qу |
| GAGCGGTTTAG 1958 | 9 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | 1899 | В |
| 555 | | 555 | Qy |
| GGCCACCTCTT 1898 | 9 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG | 1839 | DЬ |
| 555 | 5 | 555 | Qγ |
| TACAAACCAAA 1838 | 9 ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA | 1779 | DЬ |
| 555 | | 555 | Qy |
| STTTGTATTTG 1778 | 9 AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG | 1719 | Db |
| 555 | 5 | 55. | Qy |
| GAAATACCTCA 1718 | | 1660 | Db |
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| lyProLeuHis 540 | | 521 | V 0 |
| hrArgThrLeu 520 CAAGGACCCTT 1599 | 1 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu | 501 1540 | Db dg |
| ACTGTGACCCC 1539 | O AAGCGAGAGATAGTTGGGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC | 1480 | DЬ |
| yrCysAspPro 500 | | 481 | Qy |
| rpTrpGluMet 480 GTGGGAGATG 1479 | 1 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | 461 1420 | Ωy |
| AGAAGTGGAGG 1419 | | 1360 | Вb |
| luLysTrpArg 460 | 1 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 441 | Qy |
| snPheLeuLeu 440 ACTTCCTGCTC 1359 | 1 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 1300 | DP QA |
| ATTTAAAATCC 1299 | | 1240 | Db |
| isLeuLysSer 420 | 1 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | 401 | Qy |
| | 0 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGGCTAATGAAGGATTC | 1180 | Db |
| snGluGlyPhe 400 | 1 TyraspMetAlaTyralaAlaGlnProPheLeuLeuArgAsnGlyAlaA | 38: | Qγ |
| GCATATCCAG 1179 | 0 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATGAGATGGGGGCATATCCAG | 1120 | DЪ |
| lyHisileGln 380 | | 361 | Qу |
| rgIleLeuMet 360 :::::::::::::::::::::::: | 1 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet | 341 1060 | Qу |
| GAAATGTTCAG 1059 | U CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG | 1000 | מט |

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GENERAL INFORMATION:
APPLICANT: Baker, Kevi
APPLICANT: Beresini,
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APPLICANT: Cao, Wei-C
APPLICANT: Goodbard, p
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Godowski, Paul J.
Gurney, Austin L.
 Tumas,Daniel
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC251
CURRENT APPLICATION UNMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapper or Paymond Pa
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                 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
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| 1778 | AATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG | نسر | DЬ |
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| 555 1718 | CysAsp11eSerAsnSerThrGluAlaGlyGlnLysLeuPhe | 1660 | Dp Qq |
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| - 51 | | 1540 521 | Ov Ov |
| 1539 520 | laSerLeuPheHisValSerAsnAspTyrSerPheIleArqTyrTyrThrArqThrLeu | 50 | VQ |
| 1 0 | leValGlyValValGluProValProHisAspGluThrTyrCysAspPro | 481 1480 | g Qy |
| | GAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG | | 뫄 |
| m | rpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | 461 | Qy |
| 460 1419 | rlevalGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg | 1360 | Db Qy |
| iu | TGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC | 1300 | р В |
| 40 | leGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | 421 | Qy |
| 1299 | CTGTTGGGGAAATCATGTCACTTT | | B : |
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| 1179 | 3ACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCC | | Db . |
| 0 | ThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlvHisTleG | 361 | ρ |
| 360 1119 | lCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLe | 341 1060 | B 64 |
| 1059 | TGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAA | 1000 | Дb |
| 340 | roAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGl | 321 | Qy |
| 9 | GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGA | | 뫄 |
| N | laTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLe | 301 | ρ |
| ωi | | | Дb |
| 0 | euThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGl | 281 | γQ |
| 879 | TGCCTCCTGCTCATTIGCTTGGTGATATGTGGGGTAGATTTGGACAAATCTGTACTCTTGTACTCTTGTAGATATGTGTAGATTTTGGACAAATCTGTAGTCATATGTGTGGGGTAGATTTTGGACAAATCTGTAGTCTTGTAGATTAGTAGATTTTGGACAAATCTGTAGTGTGAGATTTTGGACAAAATCTGTAGTGTAGATTAGTAGAAATTTGTAGAAAAATCTGTAGTAGAATTTGTAGAAAAAATCTGTAGTAGAAATTGTGTAGAAATTTGTAGAAAAAAAA | 820 | 망 5 |
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| - 6 | HisAlaTyrValArgAlaLysLeumetAsnAlaTyrProSerTyrIleSerProIleGly HisAlaTyrValArgAlaLysLeumetAsnAlaTyrProSerTyrIleSerProIleGly | 241 760 | p Q |
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| 805 285 7 | 85 pIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPh | Ф |
| 785 2797 | 765 eArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAs . | Qу Дъ |
| 765 2737 | 745 1PheGlyValValMetGlyValI1eValValGlyI1eValI1eLeuI1ePheThrGlyI1 | Оу |
| 745 2677 | 725 uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa | р Ор |
| 725 2617 | 05 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe | Qу |
| 705 2557 | 85 IThrAlaProLysAsnValSerAspIleIleProArgThrGluValGluLysAlaIleAr | Дb |
| 685 2497 | 65 eGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheVa | DB QY |
| 665 2437 | 45 rSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh | DP QV |
| 645 2377 | 25 SSErAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe | Db Qy |
| 625 2317 | 606 TrpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy | DP QA |
| 605 2257 | 86 ASDTYFPheGLUProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGly | Дb |
| 585 2197 | ob TIPTITI JOHAL ALEUG LIASHWALVALGIYALALYSASHMETASHVALATGPYOLEULEU | g 4 |
| <u> </u> | 79 AAGGCCCTGAACCCCCTTTTTTGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCC | g dd . |
| 2078 | TAAATATATGTACATCTGGAACCCCTCAA snMetLeuArgLeuGlvLvsSerGluPro | S B |
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| 2018 | 1959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA | DЪ |
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| 1958 | 1899 TICTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | 망 |
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APPLICANT: Beresini, Mauree
APPLICANT: Desorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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LENGTH: 37
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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| 61 ASDMETASDASDALGGINASPLYSTEPSETALAPHELEULYSGLUGINSETTHILEUALA 80 |
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| | v 645 | Q _V |
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| GGAACGACAA | 231 | Db |
| SerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgS | 62 | γQ |
| CAAAGCATCAAAGTGAGGATAAGCC | 225 | Db |
| rpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLe | 60 | Qy |
| 2198 AACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGA 2257 | 219 | Db |
| nTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValG | 58 | Qy |
| GGACCCTAGCATTGGAAAATGTTGTAGGAGC-AAGAACATGAATGTAAGGCCACTGCT | 213 | ДĎ |
| pThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeu | 56 | Qy |
| 2079 AAGGCCCTGAACCCCCTTTTTTGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCC 2138 | 207 | ДĎ |
| snMetLeuArgLeuGlyLysSerGluPr | 55 | QΥ |
| 2019 GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCCTCAA 2078 | 201 | Db |
| 555 555 | 55 | Qy |
| 1959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018 | 195 | Дb |
| 555 555 | 55 | Qy |
| 1899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA | 189 | Db |
| 555 | 55 | Qy |
| 1839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG | 183 | Дb |
| 555 | 55 | Qy |
| 1779 ATTTCTTTGTTCTAAAAAGAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838 | 177 | Db |
| 555 555 | 55 | Qy |
| 1719 AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778 | 171 | Db |
| 555 555 | 55 | Qγ |
| 1660 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTT-GTAAGAAATACCTCA 1718 | 166 | Db |
| sCysAspIleSerAsnSerThrGluAlaGlyGlnLys | 54 | νο |
| 1600 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1659 | 160 | Db |
| rGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHi | 52 | Qy |
| | 154 | qq |
| 501 AlaSerLeuPheHisValSerAsnAspTvrSerPheIleArgTvrTvrThrArgThrLeu 520 | 50 | 0 |
| | 148 | Db : |
| ${	t ArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPr}$ | 4.8 | γQ |
| 20 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGAGT 14 | 142 | 망 |
| 461 TrometValPheLvsGlvGluIleProLvsAspGlnTrometLvsLvsTrpTrpGluMet 48 | 4 | 0 |
| 60 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTAC | 136 | ДD |
| 441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 46 | 44 | γο |
| TCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCT | 130 | Db |
| leGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeu | 42 | QY |

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Sequence 2, Application US/09969384
Publication No. US20020192749A1
GENERAL INFORMATION:
APPLICANT: MODIC, et al.
TITLE OF INVENTION: Human Gene Polynucleotides, Pol
FILE REFERENCE: PT055P1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR APPLICATION NUMBER: BCT/US01/10542
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                     NAME/KEY: SITE
LOCATION: (1707)
OTHER INFORMATION: n equals a
NAME/KEY: SITE
LOCATION: (2702)
OTHER INFORMATION: n equals a
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                                                         LOCATION: (2749)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2757)
OTHER INFORMATION: n
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                            NAME/KEY: SITE
LOCATION: (2788
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TYPE: DNA
                                                                                                                                         NAME/KEY: SITE
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        INFORMATION: n equals a,t,g,
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Best Local Similarity:
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LOCATION: (2835
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OTHER INFORMATION:
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LOCATION: (2819)
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                              aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe 262
                                                                                                                                                                             uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTy 202
                                                                                                                                                                                                                                            uTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluG1 182
                                                                                               TTGGAGAGAGTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTT
                                                                                                                rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLe
                                                                                                                                                              GTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTA
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                      gGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspProAlaSe 502
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SOFTWARE: PatentIn Ver.
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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moore, et al.
                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (284)
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                          uProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeuTh
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CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 2000-05-03
NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 2638
TYPE: DNA
ORGANISM: MOUSE
FEATURE: COS
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APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
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| 480 | 461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet | Qy |
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| 1485 | ACAGGCATTGACAATTGTTGGAACACTACCGTTTACTTAC | DЬ |
| 460 | GlnAlaLeuThrTleValGlyThrLeuProPheThrTyrMetLeuGluLysTr | Qy |
| 440 1425 | 421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu | Qу |
| 420 1365 | 401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer | Qу |
| 400 1305 | 381 TyraspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe | Qy Db |
| 380 1245 | 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln | Qy |
| 360 1185 | 341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet | Qy Db |
| 340 1125 | 321 ProasnmetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln | Qу Дъ |
| 320 1065 | 301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu | Db . |
| 300 1005 | 281 LeuThrvalProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln | ОУ |
| 280 945 | 261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer | Qу |
| 260 885 | 241 HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly | ОУ |
| 240 825 | 221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu | Qy Db |
| 220 765 | 201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly | ОУ |
| 200 705 | 181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly | ОУ |
| 180 645 | 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr | ОУ |
| 160 585 | 141 CysLeuLeuCluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu | Qу |
| 140 525 | 121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu | Qу |
| 465 | ::: | Db |

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FATERIAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Piddington, Christopher S.

APPLICANT: Petrie, Charles

APPLICANT: Petrie, Charles

APPLICANT: Petrie, Charles

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME

FILE REFERENCE: 99-24C1

CURRENT APPLICATION NUMBER: US/09/978,385

CURRENT FILLING DATE: 1990-05-13

PRIOR APPLICATION NUMBER: 60/151,181

PRIOR APPLICATION NUMBER: 60/151,181

PRIOR APPLICATION NUMBER: 09/563,516

PRIOR FILING DATE: 1999-08-27

PRIOR FILING DATE: 2000-05-03

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; LOCATION: (106)...(2520)
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                                                                            APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACEZ: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952 PRIOR FILING DATE: 1999-05-13 PRIOR APPLICATION NUMBER: 60/151,181 PRIOR FILING DATE: 1999-08-27 PRIOR APPLICATION NUMBER: 09/563,516
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APPLICANT:
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Best Local Similarity:
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LENGTH: 2415
TYPE: DNA
ORGANISM: Artificial Sequence
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LOCATION: (1)...(2415)
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                            GTNMGNCCNYTNYTNAAYTAYTTYGARCCNYTNTTYACNTGGYTNAARGAYCARAAYAAR
                                            ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
                                                                                GGNAARWSNGARCCNTGGACNYTNGCNYTNGARAAYGTNGTNGGNGCNAARAAYATGAAY 1740
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OTHER INFORMATION: n = A,T,C

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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/563,516
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
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Patent No. US20020177211A1
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                                                                                                                                                                  SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Piddington, Christopher S.
APPLICANT: Petrile, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version
                       OTHER INFORMATION: This degenerate sequence encodes the amino OTHER INFORMATION: sequence of SEQ ID NO:6.
                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
                                                                       FEATURE:
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DB:
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Best Local Similarity:
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YTNACNGTNCCNTTYGCNCARAARCCNAAYATHGAYGTNACNGAYGCNATGATGAAYCAR
                  LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln
                                                                                                  CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer
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TTYYTNTTYMGNWSNWSNGTNGCNTAYGCNATGMGNAARTAYTTYWSNATHATHAARAAY 1980
                            TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
                                                                                                                           ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
                                                                                                                                                                                              AAYWSNTTYGTNGGNTGGAAYACNGARTGGWSNCCNTAYGCNGAYCARWSNATHAARGTN
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